Genetic Variation in Populations of Walleye (*Stizostedion vitreum*) from Central Alberta

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of

Walleye (*Stizostedion vitreum*)

from

Central Alberta

Prepared by:

J. E. Thomas*, C. Prozniak, R. Sandham, and H. Kirk

Dept. of Biological Sciencies. University of Lethbridge. Lethbridge, Alberta
Canada. T1K 3M4

L. Chew

Dept. of Psychology. University of Lethbridge. Lethbridge, Alberta
Canada. T1K 3M4

Vance Buchwald*

Natural Resources Service, Alberta Environment. Red Deer, Alberta
Canada. T4N 6V4

Prepared for:

Fisheries and Wildlife Mgmt. Division, Natural Resources Service, Alberta Environment
and
the Alberta Conservation Association
Alberta, Canada

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* Authors to whom all correspondence should be sent.

For copies of this report, contact:

Vance Buchwald, Area Fisheries Biologist
Natural Resources Service
Alberta Environment
Suite 404, First Red Deer Place, 4911-51 Street
Red Deer, Alberta
Canada T4N 6V4

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List of Abbreviations

BhL	Bistcho Lake
BkL	Buck Lake
BmRa	Blindman River (mixed group)
BmRb	Blindman River (native to region)
GlLa	Gull Lake (mixed group)
GlLb	Gull Lake (native to region)
GnLa	Gleniffer Lake (mixed group)
LLR	Lac La Ronge
LSL	Lesser Slave Lake
MdRa	Medicine River (mixed group)
MdRb	Medicine River (native to region)
PgLa	Pigeon Lake (mixed group)
PgLb	Pigeon Lake (native to region)
PnLa	Pine Lake (1988 year-class fish, mixed group)
PnLb	Pine Lake (resident fish)
PrL	Primrose Lake
RDRa	Red Deer River (mixed group)
RDRb	Red Deer River (native to region)
SyL	Sylvan Lake
WnL	Winefred Lake
Shp	Sheep River (bull trout outgroup)

Report Summary

Genetic differences among populations of walleye (*Stizostedion vitreum*) inhabiting various drainages in Alberta were investigated. Walleye pelvic fins were sampled and the total genomic DNA examined for random amplified polymorphic DNA (RAPD) using the polymerase chain reaction (PCR). Amplified DNA fragments were separated on polyacrylamide gels and visualized with an Applied Biosystems Automated DNA sequencer equipped with a GENESCAN™ software package. RAPD data were used to calculate genetic distance values based on Cavalli-Sforza and Nei algorithms from PHYLIP version 3.5 (Felsenstein, 1993). KITSCH and FITCH distance trees were drawn from the data using the PHYLIP programs (Felsenstein, 1993). The tree data show genetic polymorphism among walleye populations. Branching of these genetic distance trees indicates that walleye from different drainage systems in Alberta may be genetically distinct.

Specific observations relating to this study indicate that:

1. A remnant population of native walleye remained in Pigeon Lake when it was stocked with walleye from Winefred Lake between 1979 and 1984. The stocked walleye from Winefred Lake have survived and walleye recruited in Pigeon Lake since 1985 have a genotype more similar to Winefred Lake than to the native Pigeon Lake stock.
2. Walleye from Lac La Ronge and Sylvan Lake are genetically similar and appear distinct from other walleye groups. There is no evidence for selection on the walleye population introduced to Sylvan Lake from Lac La Ronge.
3. Walleye recovered from Pine Lake, that were recruits of fish introduced from Lac La Ronge, were genetically different from the source stock, suggesting that these fish were subjected to selective pressures. Walleye from Pine Lake appear to be genetically distinct from walleye in Lac La Ronge and Sylvan Lake.
4. Some of the walleye stocked into Pine Lake in 1988 appear to have survived; however, fish sampled in 1994 from the 1988 year-class appear to be mainly non-stocked fish.
5. Walleye stocks from the lower Red Deer, Medicine, and Blindman rivers are genetically different

from each other indicating that different stocks may be present in these rivers. However, the difference in genetic diversity among these groups suggests that some exchange of genetic material has occurred.

6. There appears to be some evidence that walleye stocked in Gleniffer Lake moved below Dickson Dam. The stocked fish appear to have a higher presence in the Red Deer and Blindman rivers, than in the Medicine River.

1.0 Introduction

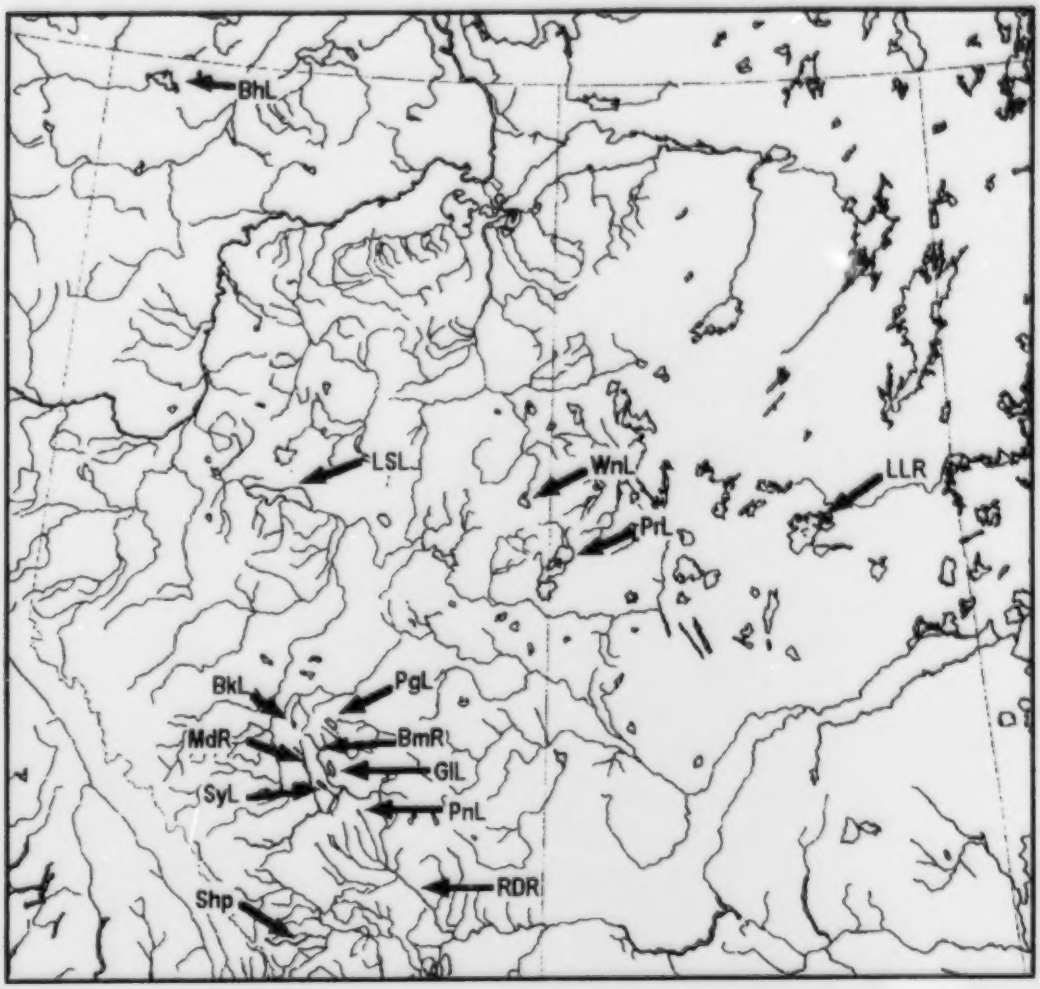
Walleye (*Stizostedion vitreum*) are native to the prairie and boreal regions of Alberta. Nelson et al. (1992) indicate that they are commonly found in both lakes and rivers and extend as far south as the South Saskatchewan and Oldman River drainages, north into the Peace, Athabasca and Slave rivers, west to the foothills and east into Saskatchewan. Stocking of walleye has occurred within some drainages either to establish new populations, or to recover existing populations. In this study we examine walleye from 13 different Alberta and Saskatchewan lakes and rivers, focussing on the Parkland Region of Alberta Environment and those sites used as egg sources for stocking.

To determine the genetic background of these fish a 10mer oligonucleotide primer (DAF1) designed by Caetano-Anolles et al. (1991) was employed; the Polymerase Chain Reaction (PCR) was used to copy and amplify Random Amplified Polymorphic DNA (RAPD) from DNA extracted from fish fins. DNA amplified by this method was visualized using an Applied Biosystems 373 automated DNA sequencer equipped with a GENESCAN™ software package. RAPD data were used to calculate genetic distance values based on Cavalli-Sforza and Nei algorithms from PHYLIP version 3.5 (Felsenstein, 1993). KITSCH and FITCH distance trees were drawn from the data using the PHYLIP programs (Felsenstein, 1993).

1.1 Study Area

The Parkland Region encompasses: part of the Red Deer River drainage system, which is a sub-basin of the South Saskatchewan River in central Alberta; the Battle River drainage, which is a sub-basin of the North Saskatchewan; and a small portion of the North Saskatchewan basin proper. Walleye were sampled from eight (8) sites within the region (Fig. 1) including the Red Deer (RDR), Medicine (MdR) and Blindman rivers (BmR). The Blindman and Medicine rivers drain into the Red Deer River and are located downstream of Gleniffer Lake below Dickson Dam, which imposes a barrier to migration of fish upstream. Walleye samples also were obtained from Gull Lake (GlL) which drains into the Blindman River; Pine (PnL) and Sylvan lakes (SyL) which drain into the Red Deer River;

Figure 1. Map of Alberta and Saskatchewan indicating the major drainages from which walleye (*Stizostedium vitreum*) were sampled.



Pigeon Lake (PgL) which is located at the north end of the region and drains into the North Saskatchewan River through Pigeon Lake Creek and the Battle River; and Buck Lake (BkL) which is located in the northwest corner of the region and drains into the North Saskatchewan River through Buck Lake Creek.

Walleye were also sampled from sites used as sources of eggs for stocking purposes. Samples were collected from Lesser Slave Lake (LSL) and Winefred Lake (WnL) in the Athabasca River Drainage System of north central Alberta; from Bistcho Lake (BhL) which is located in the Laird River Basin in northwestern Alberta and; from Lac La Ronge (LLR) and Primrose Lake (PrL) which are located in north central Saskatchewan and are part of the Churchill River drainage.

1.2 Objectives

General objectives of this study were: 1) to characterize the degree of genetic variation in walleye from the Parkland Region of Alberta; 2) to compare genotypes within the Parkland Region with genotypes from walleye populations used for stocking within the Parkland Region and; 3) to determine the influence of stocked fish on native walleye in the Parkland Region. Specific questions addressed within the study were:

1. Did walleye stocked into Pigeon Lake from Winefred Lake in 1979, 1980, 1982, 1983 and 1984 survive and was there evidence of a remnant population of native walleye in Pigeon Lake when these stockings occurred?
2. Walleye populations in Pine and Sylvan lakes were established with walleye stocked from Lac La Ronge in the early 1960s. Are walleye from Pine Lake, Sylvan Lake and Lac La Ronge genetically different from one another?
3. Did walleye stocked into Pine Lake in 1988 survive?
4. The Medicine and Blindman rivers are tributaries of the Red Deer that have spawning populations of walleye that move up from the Red Deer River each spring. Do walleye from the Medicine and Blindman rivers belong to two distinct genetic stocks?

5. Did walleye stocked into Gleniffer Lake in 1988, 1989 and 1990 move below Dickson Dam and mix with walleye in the Red Deer, Medicine and Blindman rivers?
6. Did walleye stocked into Gull Lake between 1986 and 1989 survive?

2.0 Materials and Methods

2.1 Sample Collection

Pelvic fin rays from walleye and adipose fins from bull trout were removed with scissors and placed in a standard scale envelope to provide tissue for DNA analysis. After sampling, fish were released to their native habitat. Sampling data such as sex, age, weight, fork length, and date of collection were recorded on each scale envelope (Appendix 1).

Samples from Pine Lake, Gull Lake, Pigeon Lake, Medicine River, Blindman River and the Red Deer River where broken into two groups – mixed (may contain stocked or non-stocked fish) fish and non-stocked fish (native or naturalized resident). Using the age of the walleye and the year the sample was collected (Appendix 1), the year-class of the sampled fish was determined. If the year-class of the sample was from the same year that walleye were stocked into that water body then the sample was placed in the mixed fish group. If the year-class of the sample was not from a year that walleye were stocked into that water body then the sample was placed in the non-stocked fish group.

2.2 DNA Analysis

2.2.1 Isolation and Purification of DNA

Dried fin samples ranging in size from 1.0 to 10.0 mg were cut into pieces smaller than 0.5 cm in diameter and placed in 15 ml polyethylene centrifuge tubes. Upon addition of 1.0 ml of TRIzol™ (Gibco/BRL, Life Technologies, Burlington, Ontario, Canada) reagent, samples were homogenized using a Kinematica CH-6010 polytron fitted with a 0.5 cm blade at a power setting of three. After 30 seconds, the samples were observed and homogenization was repeated if large pieces of tissue were still present. After homogenization samples were transferred to 1.5 ml screw-cap microcentrifuge tubes and stored overnight at -20° C. Homogenized samples were thawed and the DNA extracted as recommended in the TRIzol™ manufacturer's protocol. Purified DNA was dissolved in 100 µl of HPLC grade bottled water (Optima Water, Fisher Scientific, Fair Lawn, New Jersey, U.S.A.). The purity and yield of the DNA was assessed using a Beckman DU-65 spectrophotometer with a nucleic acid software

pack. Absorbency measurements were made at 320 nm, 280 nm and 260 nm. DNA purity was estimated from $A_{260/280}$ ratios where a value of 1.8 indicates pure DNA (Sambrook et al., 1989). The TRIzol™ extraction protocol routinely yielded DNA with $A_{260/280}$ ratios between 1.7 and 1.9.

2.2.2 PCR Amplification of RAPD Fragments

For RAPD analysis, a 10mer oligonucleotide primer (DAF1) initially designed by Caetano-Anolles et al. (1991) was used. The primer sequence was:

DAF1 5' - AAT CGG GCT G - 3'

(Caetano-Anolles et al., 1991)

RAPD fragments were amplified in 25 µl reaction volumes using a Techne Progene thermocycler. In 500 µl PCR tubes, a reaction mixture was prepared containing 250 ng of template DNA, 1.5 µl of 20 µM DAF1 primer, 2.5 µl of a PCR buffer consisting of 10 mM Tris-HCl at pH 8.3 and 50 mM KCl, 1.0 µl each of 1.25 mM dATP, dCTP, dGTP and dTTP, 1.0 µl of 0.3 µM (F)dUTP (Perkin Elmer Corporation, Applied Biosystems Division, Foster City, California, U.S.A.), 3.0 µl of 100 mM $MgCl_2$, 1.5 µl of 1.0 µg/µl bovine serum albumin (BSA), 0.5 units of Ultra Therm™ Thermophilic DNA polymerase (Bio/Can Scientific Inc., Mississauga, Ontario, Canada) and HPLC grade bottled water to make up the remaining volume. The amplification cycle consisted of an initial denaturation at 95^0 C for 5 min, followed by 28 cycles of 95^0C for 40s, 52^0 C for 30s, and 72^0 C for 60s. The amplification was completed with a final elongation at 72^0 C for 10 min. Amplified products were separated by polyacrylamide gel electrophoresis on an Applied Biosystems 373A DNA sequencer equipped with GENESCAN 672 software (Perkin Elmer Corporation, Applied Biosystems Division, Foster City, California, U.S.A.).

2.2.3 Visualization of DNA Fragments

DNA fragments were separated by polyacrylamide gel electrophoresis on an Applied Biosystems

373A DNA sequencer equipped with GENESCAN 672 software (Perkin Elmer Corporation, Applied Biosystems Division, Foster City, California, U.S.A.). A 5% native polyacrylamide gel was prepared in 12 cm well to read plates by combining 8.0 ml of GeneAmp™ Detection Gel (Perkin Elmer Corporation, Applied Biosystems Division, Foster City, California, U.S.A.), 2 ml of 10X TBE (Sambrook et al., 1989), and 30 ml HPLC grade bottled water with 400 µl fresh 10% ammonium persulfate and 20 µl of TEMED (N,N,N',N'-tetramethyl-ethylenediamine).

For each sample a 1.0 µl to 3.0 µl aliquot of fluorescently tagged PCR product was mixed with 0.5 µl of either ROX 1000 or ROX 2500 (Perkin Elmer Corporation, Applied Biosystems Division, Foster City, California, U.S.A.) plus loading dye supplied by the manufacturer to a total volume of 5.0 µl. Samples were applied to the top of the gel and then separated for 3 h to 4 h at 800 V, 40 mA, 30 Watts with a laser setting of 40 mW.

2.2.4 RAPD Analysis

After sizing, 15 DNA fragments that appeared consistently in replicate samples of the same fish were chosen for RAPD analysis. DNA fragments within 10 bp of 215, 257, 270, 294, 318, 339, 369, 542, 563, 832, 910, 1089, 1268, 1398 and 1620 bp were recorded and used to develop genetic profiles for individual fish sampled in the study. These data were used to calculate genetic distance values based on the Cavalli-Sforza algorithm from PHYLIP version 3.5 (Felsenstein, 1993). KITSCH and FITCH distance trees also were drawn from the data using the PHYLIP programs (Felsenstein, 1993).

Reinvasion of fish into the various Alberta drainages occurred after the last ice age, about 13,000 years ago (Nelson and Paetz 1992). Consequently, the genetic variation apparent among our samples was assumed primarily to be the result of genetic drift. For this reason discussion of the data primarily is based on analyses developed using the Cavalli-Sforza algorithm. Note that the distance values and resulting distance trees represent measures of genetic difference and are not intended to suggest direct phylogenetic relationships.

3.0 Results and Discussion

3.1 Walleye Genotypes Identified Using Random Amplified Polymorphic DNA

Walleye from the Parkland Region of central Alberta were compared with walleye samples from current and potential stocking sources in Alberta and Saskatchewan; i.e., samples from Buck Lake, Pigeon Lake, Medicine River, Blindman River, Sylvan Lake, Gull Lake, Pine Lake and the Red Deer River (Fig. 1) were compared with samples from Bistcho Lake, Lesser Slave Lake, Winefred Lake, Primrose Lake and Lac La Ronge. Bull trout from the Sheep River (Shp) also were included in the study as an outgroup for calculation of genetic distances.

A summary of DNA fragments identified in this study using the DAF1 probe is shown in Table 1. Based on the presence or absence of fifteen different DNA fragments in RAPD profiles, 171 different walleye genotypes were identified. Of these, 104 different genotypes were identified in the Parkland Region (Table 2), while 67 different walleye genotypes were identified for other lakes sampled within northern Alberta and Saskatchewan. Of these genotypes, all but 19 were unique to single fish characterized within the study (Table 1). Some overlap among genotypes from the Parkland Region and recognized fish stocking sources in northern Alberta and Saskatchewan was observed (Table 2); e.g. some genotypes from fish found in Lac La Ronge, Saskatchewan (genotypes M, T, 2A and 2D) also were found for fish from Pine Lake and Sylvan Lake in the Parkland Region. Note that both Pine Lake and Sylvan Lake originally were stocked with fish from Lac La Ronge (Appendix 1). Only one genotype appeared in three lakes; i.e. genotype M appeared in each of Pine Lake, Lac La Ronge and Bistcho Lake. No overlap of genotypes with the bull trout outgroup from the Sheep River was observed. A summary of genotypes showing individual DNA fragments determined for fish from each of the different geographical regions is presented in Table 3.

The frequency of individual DNA fragments that were used to generate the genotype data from fish within each region also were used to calculate genetic distance values for the RAPD profiles (Table 4).

Table 1. RAPD profiles generated with the DAF1 primer developed by Caetano-Anolles et al. (1991). The number of regions in which each profile was found also is shown. Fragment sizes are shown in bp in the top row. All profiles are from walleye *(Stizostedion vitreum)*, except those from 7P through 7X, which were from bull trout *(Salvelinus confluentus)*.

Profile Co	Regior	215	257	270	294	318	339	369	542	583	832	910	1089	1268	1398	1620
A	1			X	X		X		X		X	X				
B	1	X		X	X	X		X	X			X	X		X	X
C	1	X		X	X				X	X		X	X			
D	1			X	X			X	X		X	X			X	X
E	1	X	X	X	X	X		X	X	X	X	X	X			X
F	1	X		X	X		X									
G	1	X	X	X	X	X	X	X	X		X	X	X		X	
H	1		X	X	X	X		X		X	X	X	X			
I	1	X		X	X	X	X	X	X			X	X			
J	1			X			X	X	X			X			X	X
K	2	X		X	X		X			X					X	
L	1	X		X	X		X		X	X	X					X
M	3	X		X	X		X	X	X	X					X	
N	2	X	X	X	X		X		X	X			X			
O	4	X	X	X	X		X		X	X						
P	1	X	X	X	X		X	X		X	X				X	X
Q	1		X	X		X		X		X	X	X	X		X	X
R	2		X	X	X	X		X		X	X	X	X		X	X
S	1	X	X	X	X	X	X	X			X	X	X		X	X
T	3	X		X	X		X	X		X	X	X	X		X	X
U	2	X	X	X	X	X	X	X		X	X	X	X		X	X
V	1	X	X	X	X	X		X			X	X	X			X
W	1			X	X	X				X	X	X	X		X	
X	1	X	X	X	X	X		X		X	X	X				X
Y	1	X		X	X			X			X	X			X	X
Z	1		X		X	X			X	X	X	X	X		X	
2A	2	X		X	X		X	X		X	X		X		X	X
2B	1	X		X	X		X	X		X	X				X	X
2C	1	X		X	X		X			X	X	X			X	X
2D	3	X		X	X		X	X		X		X			X	X
2E	1	X		X	X		X		X			X				
2F	1	X		X	X		X	X			X	X	X			X
2G	1	X	X	X	X		X	X	X			X	X		X	X
2H	1			X	X	X			X		X	X	X		X	X
2I	1			X	X					X	X	X				
2J	1				X	X	X	X	X		X				X	X
2K	1	X	X	X	X	X		X		X	X	X	X		X	X
2L	1			X	X	X	X	X	X		X		X		X	X
2M	2			X	X	X	X	X	X		X	X	X		X	X
2N	1	X		X	X	X	X	X	X				X		X	
2O	1				X	X	X	X		X	X	X			X	
2P	1	X			X			X			X	X	X			
2Q	1	X			X		X				X	X	X			
2R	1	X	X	X		X	X					X	X			
2S	1	X		X	X		X					X	X			
2T	1	X				X	X		X	X		X	X			X
2U	1	X	X		X	X					X	X	X			
2V	1		X	X		X			X							
2W	1					X						X			X	
2X	1	X		X	X	X					X		X		X	X
2Y	1		X			X	X	X		X	X					
2Z	1	X	X	X	X	X	X	X	X	X	X	X	X			
3A	1	X		X				X	X		X		X			
3B	1		X			X		X	X		X	X				
3C	3	X		X	X			X	X		X	X				
3D	1	X		X		X		X								
3E	1			X	X			X	X		X	X	X		X	

Profile Co	Region	215	257	270	294	318	339	369	542	563	832	910	1089	1268	1398	1620
3F	2	X		X	X		X	X	X		X	X				
3G	1	X		X				X			X					X
3H	1	X		X				X	X		X	X				
3I	2	X		X			X		X		X					
3J	1			X				X	X		X	X				
3K	1	X		X	X	X		X			X	X				
3L	1	X		X	X		X			X	X	X			X	
3M	1	X		X			X			X	X		X			
3N	1	X		X	X	X					X	X				X
3O	1	X		X	X		X	X		X			X			
3P	1			X	X		X	X	X		X	X				
3Q	1	X			X				X		X	X				
3R	1	X		X	X			X	X			X				
3S	1				X			X	X	X	X	X				
3T	1	X			X		X	X	X		X	X				
3U	1	X	X	X	X		X	X					X		X	
3V	2	X	X	X	X		X	X	X	X			X		X	
3W	2	X	X	X	X		X	X		X			X		X	X
3X	1	X	X	X	X	X	X	X	X	X	X				X	X
3Y	1	X	X	X	X	X	X	X	X	X					X	X
3Z	1	X	X	X	X	X	X	X		X	X		X		X	X
4A	1	X	X	X	X		X	X		X					X	X
4B	1	X	X	X	X			X	X		X	X	X			X
4C	1	X	X	X	X	X	X	X		X	X	X	X			
4D	1	X	X	X	X		X	X	X		X	X				
4E	1	X		X	X		X	X	X	X	X	X	X			X
4F	1	X		X	X	X		X		X	X	X				X
4G	1	X	X		X		X		X		X					
4H	1	X	X	X	X		X		X	X		X				X
4I	1	X	X	X	X		X									
4J	1	X	X		X	X		X	X							
4K	1	X		X	X		X	X	X						X	
4L	1	X		X	X	X	X	X	X			X	X			X
4M	1	X		X	X	X	X	X	X		X	X	X		X	
4N	1	X		X	X	X	X	X	X		X	X	X			X
4O	1	X		X	X		X	X	X		X	X	X		X	X
4P	1	X		X	X		X	X	X		X	X	X			
4Q	1	X	X	X	X		X	X	X		X	X	X			X
4R	1	X	X	X	X	X	X	X		X	X	X	X	X	X	X
4S	1			X			X	X		X	X	X	X			X
4T	1	X	X	X	X	X	X	X				X				X
4U	1	X	X		X		X					X	X	X	X	
4V	1	X		X	X		X	X	X					X		
4W	1	X		X	X		X		X					X		
4X	2	X		X	X		X		X	X						
4Y	1	X		X	X		X					X				
4Z	2	X		X	X		X		X	X			X			
5A	1	X	X	X	X	X	X	X		X					X	X
5B	1		X		X	X		X	X		X	X	X		X	X
5C	1	X		X	X	X	X	X				X	X			X
5D	1			X	X			X	X	X	X	X	X		X	X
5E	1	X		X	X		X	X		X					X	X
5F	1	X		X	X		X	X	X						X	X
5G	1	X	X	X	X		X	X		X	X	X	X		X	X
5H	1	X		X	X		X	X		X			X		X	X
5I	1		X	X	X		X	X		X	X	X	X		X	
5J	1	X		X	X	X	X	X		X	X				X	X
5K	1	X		X	X	X				X	X	X	X		X	X
5L	1	X		X	X			X			X	X	X		X	X
5M	1				X			X	X		X	X	X		X	X
5N	1	X	X	X	X		X	X		X	X	X	X			
5O	1	X	X	X	X		X	X		X			X			
5P	1	X		X	X		X	X		X	X	X	X			X
5Q	1	X	X	X	X	X	X	X			X			X		X
5R	1	X	X		X		X	X		X			X			X
5S	1	X	X	X	X		X	X		X	X					X

Profile Co	Region	215	257	270	294	318	339	369	542	563	832	910	1089	1268	1398	1620
5T	1	X		X	X		X	X			X					X
5U	1	X		X	X		X	X		X	X					X
5V	1	X		X	X	X		X			X					
5W	1	X	X		X		X	X		X	X					X
5X	1			X	X		X									
5Y	1	X		X	X		X	X		X		X				X
5Z	1	X	X	X			X				X	X				
6A	1	X	X	X	X		X			X			X		X	X
6B	1			X	X		X	X								
6C	1	X	X	X	X		X		X		X	X				
6D	3	X		X	X		X	X	X	X						
6E	1	X	X		X		X		X		X	X	X		X	X
6F	1	X	X		X		X		X	X					X	
6G	1	X	X		X		X		X	X		X	X		X	
6H	1	X	X	X	X		X	X				X	X		X	
6I	1	X	X	X	X		X						X		X	X
6J	1	X	X	X	X		X	X	X				X			X
6K	1		X		X				X			X				
6L	1	X	X		X			X		X		X			X	X
6M	1	X	X	X	X		X			X		X	X		X	
6N	1	X	X		X	X	X					X		X	X	X
6O	1	X	X				X		X	X		X			X	
6P	1	X	X	X	X		X	X	X			X				
6Q	1	X	X		X		X	X	X	X	X				X	X
6R	1	X	X		X	X			X	X						
6S	1	X	X	X	X		X	X	X	X			X			
6T	1	X	X	X	X		X	X	X			X		X	X	
6U	1	X	X	X	X		X						X		X	
6V	1	X	X	X	X		X						X	X	X	
6W	1	X		X	X		X	X	X	X			X			
6X	2	X	X	X	X		X	X	X	X						
6Y	1	X		X	X	X	X	X	X	X			X			
6Z	1	X	X		X		X		X	X		X				
7A	1	X		X	X		X		X		X		X			
7B	1	X	X	X	X		X			X	X	X				X
7C	1	X	X		X		X			X		X	X		X	X
7D	1	X	X	X	X		X					X			X	X
7E	1	X	X	X	X		X	X	X						X	
7F	1	X	X		X		X	X	X			X				X
7G	1	X	X	X	X		X			X		X			X	X
7H	1	X	X		X		X		X	X						
7I	1	X		X	X		X	X		X		X	X		X	
7J	1	X		X	X		X	X	X	X		X	X		X	X
7K	1	X		X	X		X		X	X		X	X		X	X
7L	1	X	X				X		X	X			X		X	
7M	1	X		X	X	X		X	X	X			X		X	
7N	1	X	X	X	X		X			X		X	X		X	X
7O	1	X		X	X							X	X		X	X
7P	1		X			X			X				X	X		
7Q	1		X			X										
7R	1		X			X	X		X							
7S	1		X					X		X			X			
7T	1		X			X			X				X	X		
7U	1		X			X			X				X	X		X
7V	1		X			X			X				X	X		
7W	1		X					X		X						
7X	1		X			X			X				X	X		

Table 2. Summary of RAPD profiles found in each region. All profiles were obtained from walleye (*Stizostedion vitreum*), except those from Sheep River which were bull trout (*Salvelinus confluentus*). Lower case a/b divide populations into groups: mixed (may contain stocked or non-stocked) fish (a) and non-stocked fish (b).

Pine Lake (a): A,B,C,D, F,K,L,M,N,O

Pine Lake (b): E,F,G,H,I,J

Buck Lake: P,Q,R,S,T,U,V,W

Sylvan Lake: T,X,Y,Z,2A,2B,2C,2D,2E,2F

Medicine River (a): 2G,2H,2I,2J,2Q,2R,2S,2U

Medicine River (b) and Little Red Deer River: 2K,2L,2M,2N,2O,2P,2T,2V,2W, 2X,2Y,2Z

Gull Lake (a): 3A,3B,3C,3D,3E,3F

Gull Lake (b): 3G,3H,3I,3J,3K,3L,3M,3N,3O

Blindman River (a): 3C,3F,3P,3Q,3R

Blindman River (b): 3C,3S,3T,3U,3V

Red Deer River (a): 3W,3X,3Y,4I,4J,4K

Red Deer River (b): O,3Z,4A,4B,4C,4D,4E,4F,4G,4H

Pigeon Lake (a): 4L,4M,4N,4U,4V,4W,4X,4Z

Pigeon Lake (b): 2M,4O,4P,4Q,4R,4S,4T,4Y

Lac La Ronge: M,R,T,U,2A,2D,3W,5A,5B,5C,5D,5E,5F,5G,5H,5I,5J,5K,5L,5M,5N

Primrose Lake: 5O,5P,5Q,5R,5S,5T,5U,5V,5W,5X,5Y,5Z,6A,6B

Winefred Lake: 2D,6C,6D,6E,6F,6G,6H,6I,6J,6K,6L,6M,6N,6O,6P,6Q,6R,6S,6T

Bistcho Lake: M,N,O,3I,3V,4Z,6D,6U,6V,6W,6X,6Y,6Z,7A

Lesser Slave Lake: K,O,4X,6D,6X,7B,7C,7D,7E,7F,7G,7H,7I,7J,7K,7L,7M,7N,7O

Sheep River: 7P,7Q,7R,7S,7T,7U,7V,7W,7X

Table 3. Fragment band pattern for walleye (*Stizostedion vitreum*) samples. Each DNA fragment (in base pairs) found in a sample is marked by an "X". The (A) and (B) designations divide the samples into groups thought to be composed of stocked fish (A) and non-stocked fish (B). All samples were walleye, except those from the Sheep River which were bull trout (*Salvelinus confluentus*).

	215	257	270	294	318	339	369	542	563	832	910	1089	1268	1398	1620
Pine Lake (A)															
W24			X	X		X		X		X	X				
W26	X		X	X	X		X	X			X	X		X	X
W27	X		X	X				X	X		X	X			
W30			X	X			X	X		X	X			X	X
W201	X		X	X		X			X					X	
W202	X		X	X		X									X
W203	X		X	X		X		X	X	X					
W204	X		X	X		X	X	X	X						X
W205	X	X	X	X		X		X	X			X			
W206	X	X	X	X		X		X	X						
Pine Lake (B)															
W1	X	X	X	X	X		X	X	X	X	X	X			X
W23	X		X	X		X									
W25	X	X	X	X	X	X	X	X		X	X	X		X	
W28		X	X	X	X		X		X	X	X	X			
W29	X		X	X	X	X	X	X			X	X			
W31			X			X	X	X			X			X	X
Buck Lake															
W2 Did not amplify															
W5	X	X	X	X		X	X		X	X				X	X
W6		X	X		X		X		X	X	X	X		X	X
W7		X	X	X	X		X		X	X	X	X		X	X
W8	X	X	X	X	X	X	X		X	X	X	X		X	X
W9	X		X	X		X	X			X	X	X		X	X
W10	X	X	X	X	X	X	X		X	X	X	X		X	X
W11	X	X	X	X	X		X			X	X	X		X	X
W21			X	X	X				X	X	X	X			X
W22 Did not amplify														X	
Sylvan Lake															
W3	X	X	X	X	X		X		X	X	X				
W12	X		X	X		X	X		X	X	X	X			X
W13	X		X	X			X			X	X			X	X
W14		X		X	X					X	X			X	X
W15	X		X	X		X	X		X	X	X	X		X	
W16	X		X	X		X	X		X	X		X		X	X
W17	X		X	X		X			X	X				X	X
W18	X		X	X		X	X		X	X	X			X	X
W19	X		X	X		X	X		X		X			X	X
W20	X		X	X		X	X			X	X	X			
															X
Medicine River (A)															
W35	X	X	X	X		X	X	X			X	X		X	X
W36			X	X	X			X		X	X	X		X	X
W38			X	X					X	X	X				
W40				X	X	X	X	X		X					
W188	X			X		X				X	X	X		X	X
W187	X	X	X		X	X					X	X			
W188	X		X	X		X					X	X			
W190	X	X		X	X					X	X	X			
Medicine River (B)															
W4	X	X	X	X	X		X		X	X	X	X		X	X
W32			X	X	X	X	X	X		X		X		X	X
W33			X	X	X	X	X	X			X	X		X	X
W34	X		X	X	X	X	X	X		X	X	X		X	X
W37				X	X	X	X					X		X	
W39	X			X			X		X	X	X			X	
W189	X				X	X		X	X		X	X			
W191		X	X		X			X							X
W192					X						X				
W193	X		X	X	X					X		X		X	X

	215	257	270	294	318	339	369	542	563	832	910	1089	1268	1398	1620
Little Red Deer R															
W71		X			X	X	X		X	X					
W72	X	X	X	X	X	X	X	X	X	X	X	X			
Gull Lake (A)															
W41	X		X			X	X		X			X			
W42		X			X	X	X			X	X				
W44	X		X	X		X	X		X	X					
W46	X		X		X	X									
W49			X	X		X	X		X	X	X			X	
W50	X		X	X		X	X	X		X	X				
Gull Lake (B)															
W43	X		X			X			X						
W45	X		X			X	X		X	X					X
W47	X		X		X		X		X						
W48			X			X	X		X	X					
W194 Did not amplify															
W195	X		X	X	X		X			X	X				
W196	X		X	X		X			X	X					
W197 Did not amplify														X	
W198	X		X			X		X	X		X				
W199	X		X	X	X				X	X					X
W200	X		X	X		X	X		X		X				
Blindman R (A)															
W51			X	X		X	X	X		X	X				
W52	X		X	X			X	X		X	X				
W53	X		X	X			X	X		X	X				
W54	X			X				X		X	X				
W55	X		X	X			X	X		X	X				
W58	X		X	X			X	X			X				
W59	X		X	X		X	X	X		X	X				
Blindman R (B)															
W56				X			X	X	X	X	X				
W57	X			X		X	X	X		X	X				
W60	X		X	X			X	X		X	X				
W179	X	X	X	X		X	X								
W180	X	X	X	X		X	X	X	X			X		X	
												X		X	
Red Deer River (A)															
W62	X	X	X	X		X	X		X						
W64	X	X	X	X	X	X	X	X	X	X		X		X	X
W65	X	X	X	X	X	X	X	X	X					X	X
w210	X	X	X	X		X	X	X	X					X	X
w211	X	X		X	X		X	X							
w212	X		X	X		X	X	X							
														X	
Red Deer River (B)															
W61	X	X	X	X	X	X	X		X	X		X			
W63	X	X	X	X		X	X		X					X	X
W66	X	X	X	X			X		X					X	X
W67	X	X	X	X	X	X	X			X	X	X			X
W68	X	X	X	X		X	X	X	X	X	X	X			
W69	X		X	X		X	X	X	X	X					
W70	X		X	X	X		X	X	X	X	X	X			X
w207	X	X	X	X		X		X	X						X
w208	X	X		X		X		X		X					
w209	X	X	X	X		X		X	X		X				X

	215	257	270	294	318	339	389	542	563	832	910	1089	1268	1398	1620
Pigeon Lake (A)															
W73	X		X	X	X	X	X	X			X	X			X
W74	X		X	X	X	X	X	X		X	X	X		X	
W75	X		X	X	X	X	X	X		X	X	X			X
W181	X	X		X		X					X	X	X	X	
W182	X		X	X		X	X	X					X		
W183	X		X	X		X		X					X		
W184	X		X	X		X		X	X						
W213	X		X	X		X		X	X			X			
Pigeon Lake (B)															
W76	X		X	X		X	X	X		X	X	X		X	X
W77	X		X	X		X	X	X		X	X	X			
W78	X	X	X	X		X	X	X		X	X	X			X
W79			X	X	X	X	X	X		X	X	X		X	X
W80	X	X	X	X	X	X	X		X	X	X	X	X	X	X
W81			X			X	X		X	X	X	X			X
W82	X	X	X	X	X	X	X				X				X
W185	X		X	X		X					X				
L L Ronge															
W83	X		X	X		X	X		X		X			X	X
W84	X	X	X	X		X	X		X			X		X	X
W85		X	X	X	X		X		X	X	X	X		X	X
W86	X		X	X		X	X		X	X	X	X		X	X
W87	X	X	X	X	X	X	X		X					X	X
W88		X		X	X		X	X		X	X	X		X	X
W89	X	X	X	X	X	X	X		X	X	X	X		X	X
W90	X		X	X		X	X		X	X		X		X	X
W91	X		X	X	X	X	X				X	X			X
W92			X	X			X	X	X	X	X	X		X	X
W93	X		X	X		X	X		X					X	X
W94	X		X	X		X	X	X						X	X
W95	X	X	X	X		X	X		X	X	X	X		X	X
W96	X		X	X		X	X		X			X		X	X
W97		X	X	X		X	X		X	X	X	X		X	
W98	X		X	X	X	X	X		X	X				X	X
W99	X		X	X	X				X	X	X	X		X	X
W100	X		X	X			X			X	X	X		X	X
W101	X		X	X		X	X	X	X					X	
W102				X			X	X		X	X	X		X	X
W103	X	X	X	X		X	X		X	X	X	X			
Winefred Lake															
W119	X	X	X	X		X		X		X	X				
W120	X		X	X		X	X	X	X						
W121	X	X		X		X		X		X	X	X		X	X
W122	X	X		X		X		X	X					X	
W123	X	X		X		X		X	X			X		X	
W124	X	X	X	X		X	X				X	X		X	
W125	X	X	X	X		X						X		X	X
W126	X	X	X	X		X	X	X				X			X
W127	X		X	X		X	X		X		X			X	X
W128		X		X				X			X				
W129	X	X		X			X		X		X			X	X
W130	X	X	X	X		X			X		X	X		X	
W131	X	X		X	X	X					X		X	X	X
W132	X	X				X		X	X		X			X	
W133	X	X	X	X		X	X	X			X				
W134	X	X		X		X	X	X	X	X				X	X
W135	X	X		X	X			X	X						
W136	X	X	X	X		X	X	X	X			X			
W137	X	X	X	X		X			X		X	X		X	
W138	X	X	X	X		X	X	X			X		X	X	

	215	257	270	294	318	339	389	542	563	832	910	1089	1268	1398	1620
Bistcho Lake															
W139	X	X	X	X		X						X		X	
W140	X		X	X		X	X	X	X					X	
W141	X	X	X	X		X	X	X	X					X	
W142	X	X	X	X		X		X	X			X			
W143	X	X	X	X		X						X	X	X	
W144	X		X	X		X	X	X	X			X			
W145	X		X	X		X	X	X	X						
W146	X	X	X	X		X	X	X	X						
W147	X		X	X		X		X	X			X			
W148	X		X	X		X	X	X	X						
W149	X		X	X		X	X	X	X						
W150	X	X	X	X		X		X	X			X			
W151	X	X	X	X		X		X	X			X			
W152	X		X	X	X	X	X	X	X			X			
W153	X		X	X		X	X	X	X						
W154	X	X	X	X		X		X	X						
W155	X		X			X		X		X					
W156	X	X		X		X		X	X		X				
W157	X		X	X		X		X		X		X			
W158	X	X	X	X		X		X	X						
Lesser Slave Lake															
W159	X	X	X	X		X			X	X	X				X
W160	X		X	X		X	X	X	X						
W161	X	X		X		X			X		X	X		X	X
W162	X	X	X	X		X					X			X	X
W163	X	X	X	X		X	X	X						X	
W164	X	X		X		X	X	X			X				X
W165	X	X	X	X		X			X		X			X	X
W166	X	X		X		X		X	X						
W167	X		X	X		X	X		X		X	X		X	
W168	X		X	X		X	X	X	X		X	X		X	X
W169	X		X	X		X		X	X		X	X		X	X
W170	X	X	X	X		X	X	X	X						
W171	X		X	X		X			X					X	
W172	X	X	X	X		X		X	X						
W173	X	X				X		X	X			X		X	
W174	X		X	X	X		X	X	X			X		X	
W175	X	X	X	X		X	X	X	X						
W176	X		X	X		X		X	X						
W177	X	X	X	X		X			X		X	X		X	X
W178	X		X	X							X	X		X	X
Primrose Lake															
W104	X	X	X	X		X	X		X			X			
W105	X		X	X		X	X		X	X	X	X			X
W106	X	X	X	X	X	X	X			X			X		X
W107	X	X		X		X	X		X			X			X
W108	X	X	X	X		X	X		X	X					X
W109	X		X	X		X	X			X					X
W110	X		X	X		X	X		X	X					X
W111	X	X		X		X	X		X			X			X
W112	X		X	X	X		X			X					
W113	X	X		X		X	X		X	X					X
W114			X	X		X									
W115	X		X	X		X	X		X		X				X
W116	X	X	X			X				X	X				
W117	X	X	X	X		X			X			X		X	X
W118			X	X		X	X								
Sheep River															
Shp1		X			X			X				X	X		
Shp2		X			X										
Shp3		X			X	X		X							
Shp4		X				X			X			X			
Shp5		X			X			X				X	X		
Shp6		X			X			X				X	X		
Shp7		X			X			X				X	X		
Shp8		X			X			X				X	X		X
Shp9		X			X			X				X	X		
Shp10		X			X			X				X	X		
Shp11		X			X			X				X	X		
Shp12		X			X			X				X	X		
Shp13		X			X			X				X	X		
Shp15		X				X			X						
Shp16		X			X			X				X	X		

Table 4. Regions included in the RAPD analysis and corresponding DNA band frequencies used for calculation of genetic distance values. The top row indicates targeted DNA fragment sizes in bp and values below show the *frequency of DNA bands in each sample. All samples were walleye (Stizostedion vitreum)*, except those from Sheep River which were bull trout (*Salvelinus confluentus*). A / B divide populations into groups thought to be composed of stocked fish (A) and non-stocked fish (B).

	215	257	270	294	318	339	369	542	563	832	910	1089	1268	1398	1620
Pine Lake (A)	0.800	0.200	1.000	1.000	0.100	0.700	0.300	0.800	0.600	0.300	0.400	0.300	0.000	0.400	0.300
Pine Lake (B)	0.667	0.500	1.000	0.833	0.667	0.667	0.833	0.667	0.333	0.500	0.833	0.667	0.000	0.333	0.333
Buck Lake	0.625	0.750	1.000	0.875	0.750	0.500	0.875	0.000	0.750	1.000	0.875	0.875	0.000	0.875	0.875
Sylvan Lake	0.900	0.200	0.900	1.000	0.200	0.700	0.700	0.200	0.700	0.800	0.800	0.400	0.000	0.700	0.800
Medicine R. (A)	0.625	0.375	0.625	0.875	0.500	0.625	0.250	0.375	0.125	0.625	0.875	0.750	0.000	0.375	0.375
Medicine R. (B)	0.500	0.200	0.600	0.700	0.900	0.500	0.600	0.500	0.300	0.600	0.600	0.700	0.000	0.700	0.500
Gull Lake (A)	0.667	0.167	0.833	0.500	0.333	0.167	1.000	0.833	0.000	0.833	0.667	0.333	0.000	0.167	0.000
Gull Lake (B)	0.889	0.000	1.000	0.444	0.222	0.444	0.556	0.333	0.333	0.889	0.556	0.222	0.000	0.111	0.222
Blindman R. (A)	0.857	0.000	0.857	1.000	0.000	0.286	0.857	1.000	0.000	0.857	1.000	0.000	0.000	0.000	0.000
Blindman R. (B)	0.800	0.400	0.600	1.000	0.000	0.600	1.000	0.800	0.400	0.600	0.600	0.400	0.000	0.400	0.000
Red Deer River (A)	1.000	0.833	0.833	1.000	0.500	0.833	0.833	0.667	0.500	0.166	0.000	0.167	0.000	0.667	0.500
Red Deer River (B)	1.000	0.800	0.900	1.000	0.300	0.800	0.700	0.600	0.700	0.700	0.600	0.400	0.000	0.200	0.600
Pigeon Lake (A)	1.000	0.125	0.875	1.000	0.375	1.000	0.500	0.875	0.250	0.250	0.500	0.625	0.375	0.250	0.250
Pigeon Lake (B)	0.750	0.375	1.000	0.875	0.375	1.000	0.875	0.500	0.250	0.750	1.000	0.750	0.125	0.375	0.750
L.L. Ronge	0.762	0.381	0.905	1.000	0.333	0.714	0.952	0.238	0.762	0.619	0.619	0.714	0.000	0.905	0.857
Primrose Lake	0.867	0.533	0.800	0.933	0.133	0.933	0.800	0.000	0.600	0.533	0.200	0.333	0.067	0.067	0.667
Winefred Lake	0.950	0.900	0.550	0.950	0.100	0.850	0.450	0.650	0.550	0.150	0.650	0.400	0.100	0.650	0.350
Bistcho Lake	1.000	0.500	0.950	0.950	0.050	1.000	0.450	0.900	0.800	0.100	0.050	0.500	0.050	0.200	0.000
Lesser Slave Lake	1.000	0.600	0.800	0.950	0.050	0.900	0.400	0.600	0.800	0.000	0.500	0.400	0.000	0.600	0.450
Sheep River	0.000	1.000	0.000	0.000	0.867	0.067	0.133	0.800	0.133	0.000	0.000	0.800	0.733	0.000	0.067

3.2 Genetic Distance Values Calculated from RAPD Profiles

Genetic distance values were calculated with the Cavalli-Sforza algorithm from PHYLIP version 3.5 (Felsenstein, 1993), which is based on a pure genetic drift model. This approach is not heavily influenced by within-taxon heterozygosity. Distance values calculated with this algorithm take on a limiting value of one regardless of the variability found within each population (Swofford et al., 1996). Consequently limited sample sizes, which often fail to produce evidence for common alleles shared between two taxa can be evaluated from a more conservative perspective. Also variances in allele frequencies are transformed in an attempt to standardize distance values such that the rate of increase in genetic distance is nearly independent of the initial gene frequencies. The genetic distance between fish in the out group and walleye from the populations under study provide some measure of the genetic distance between two species. While large genetic differences within a species may be construed as providing evidence for separate groups or populations of walleye in the analysis, these differences in themselves do not necessitate that the groups of walleye being compared actually belong to separate groups or populations. Supporting evidence based on knowledge of the morphology, physiology and / or behaviour of each of the populations being examined must also be considered.

Genetic distance values derived using the Cavalli-Sforza algorithm for walleye sampled within the Parkland Region, as well as five other lakes in northern Alberta and Saskatchewan are shown in Table 5. These values were used to derive both KITSCH (Fig. 2) and FITCH (Fig. 3) genetic distance trees. In all cases bull trout from the Sheep River (Shp), Alberta were used as an out group for comparison purposes. In all cases the bull trout genotypes segregated from the walleye 100% of the time in both KITSCH and FITCH analyses. Both genetic distance trees generated indicate that several groups of walleye may be identified as having combinations of RAPD DNA segments which are genetically distinct from DNA found in walleye from other geographical regions within Alberta and Saskatchewan; e.g. the genetic distance between walleye from Bistcho Lake and Buck Lake was 1.02 (Table 5) while that for bull trout (the out group) and walleye from the Medicine River was also 1.02. KITSCH analysis shows that RAPD profiles from fish obtained from four out of five lakes sampled in northern Alberta and Saskatchewan appear to segregate together (Fig. 2); i.e. samples from Bistcho

Table 5. Genetic distance values generated with the Cavalli-Sforza distance algorithm using PHYLIP version 3.5. All populations were walleye (*Stizostedion vitreum*) except for those from the Sheep River (Shp) which were bull trout (*Salvelinus confluentus*). Lower case a / b divide populations into groups thought to be composed of mixed (may contain stocked or non-stocked) fish (a) and of non-stocked fish (b).

	Shp	PnLa	PnLb	BkL	SyL	MdRa	MdRb	GlLa	GlLb	BmRa	BmRb	RDRa	RDRb	PgLa	PgLb	LLR	PrL	WnL	BhL
PnLa	1.2968																		
PnLb	1.2054	0.1975																	
BkL	1.7633	0.6045	0.3309																
SyL	1.7247	0.3507	0.2212	0.2479															
MdRa	1.0704	0.3048	0.1379	0.4014	0.2164														
MdRb	1.0170	0.2333	0.1427	0.3488	0.2493	0.1007													
GlLa	1.2049	0.5834	0.2799	0.7768	0.5546	0.3604	0.3583												
GlLb	1.4064	0.3951	0.2534	0.5684	0.2847	0.2821	0.3158	0.2628											
BmRa	1.8937	0.8050	0.6135	1.2742	0.7114	0.6352	0.8175	0.3243	0.4677										
BmRb	1.4294	0.5236	0.2979	0.7344	0.3383	0.3613	0.4256	0.2571	0.4142	0.3863									
RDRa	1.2982	0.3221	0.3574	0.6878	0.3640	0.4739	0.4246	0.6741	0.5845	0.9821	0.4042								
RDRb	1.4374	0.2958	0.1812	0.4122	0.1451	0.2557	0.3402	0.5257	0.3518	0.6866	0.2875	0.1995							
PgLa	1.3220	0.2941	0.2858	0.8254	0.3622	0.3131	0.3985	0.5594	0.4266	0.6556	0.3752	0.3402	0.2585						
PgLb	1.6074	0.4531	0.1451	0.3506	0.2169	0.2389	0.3229	0.5170	0.3895	0.7314	0.4597	0.5524	0.2619	0.2953					
LLR	1.6528	0.3912	0.2178	0.1949	0.0659	0.2873	0.2344	0.6117	0.4515	0.9525	0.3628	0.3245	0.2035	0.4324	0.2478				
PrL	1.3453	0.4867	0.3392	0.4632	0.2197	0.3374	0.4109	0.6263	0.3511	0.8936	0.4119	0.3108	0.1967	0.3707	0.3546	0.2678			
WnL	1.1078	0.3923	0.2722	0.6082	0.2686	0.2415	0.3381	0.5982	0.5094	0.8001	0.2806	0.2142	0.1579	0.2403	0.3657	0.2938	0.2938		
BhL	1.3141	0.4172	0.4401	1.0244	0.5420	0.5443	0.6336	0.6917	0.5357	0.8394	0.3567	0.2831	0.3140	0.2113	0.5976	0.5860	0.4072	0.2627	
LSL	1.3631	0.3718	0.3404	0.7069	0.2813	0.3590	0.4372	0.7389	0.5093	0.9032	0.3725	0.2125	0.1978	0.2634	0.4586	0.3160	0.3152	0.0857	0.1951

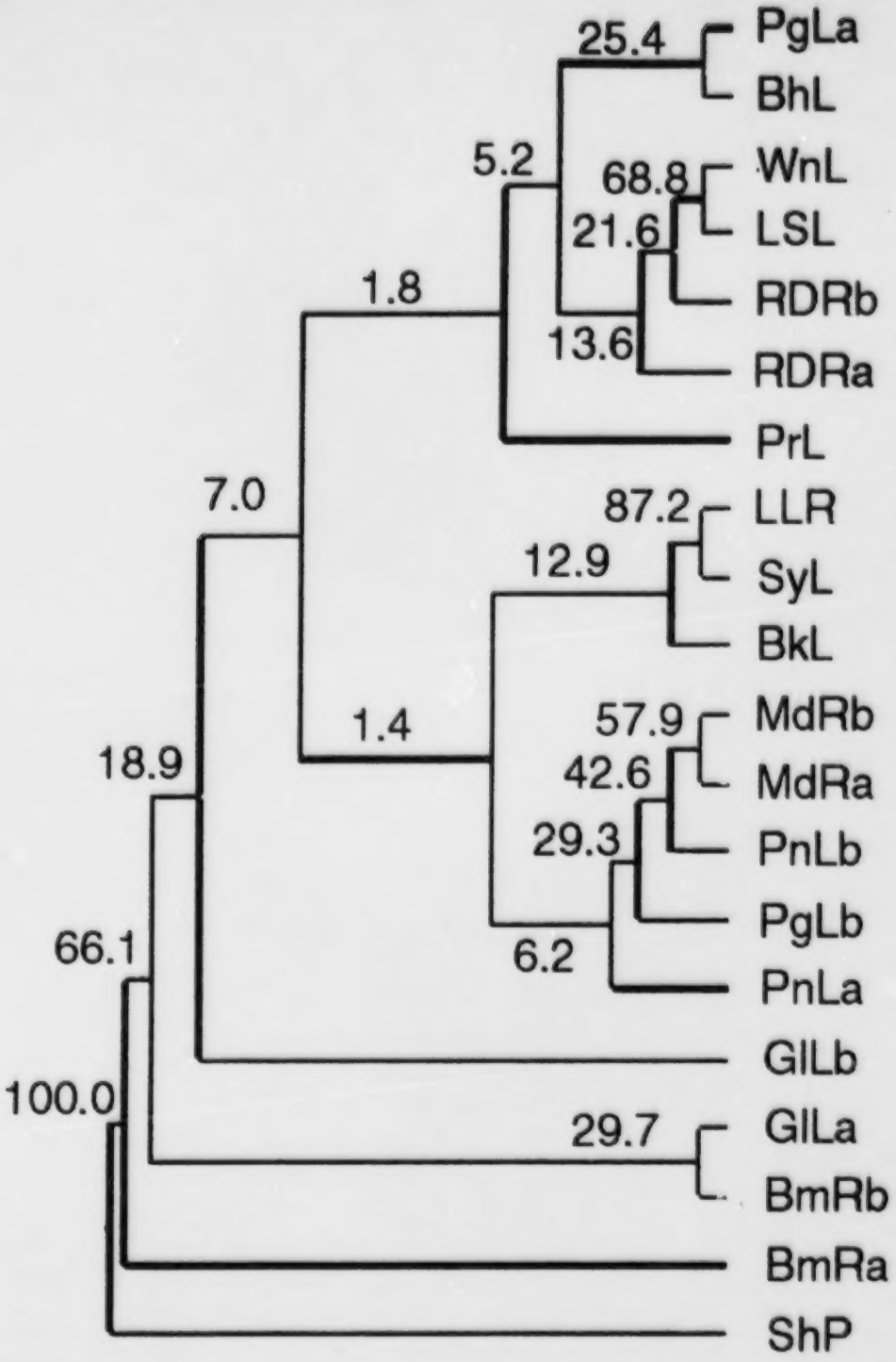


Figure 2. KITSCH tree based on Cavalli-Sforza's genetic distance values. All samples were walleye (*Stizostedion vitreum*) except those from the Sheep River (Shp) which were bull trout (*Salvelinus confluentus*). Lower case a / b divide populations into groups thought to be composed of mixed (may contain stocked or non-stocked) fish (a) and non-stocked fish (b). Numbers indicate bootstrap values.

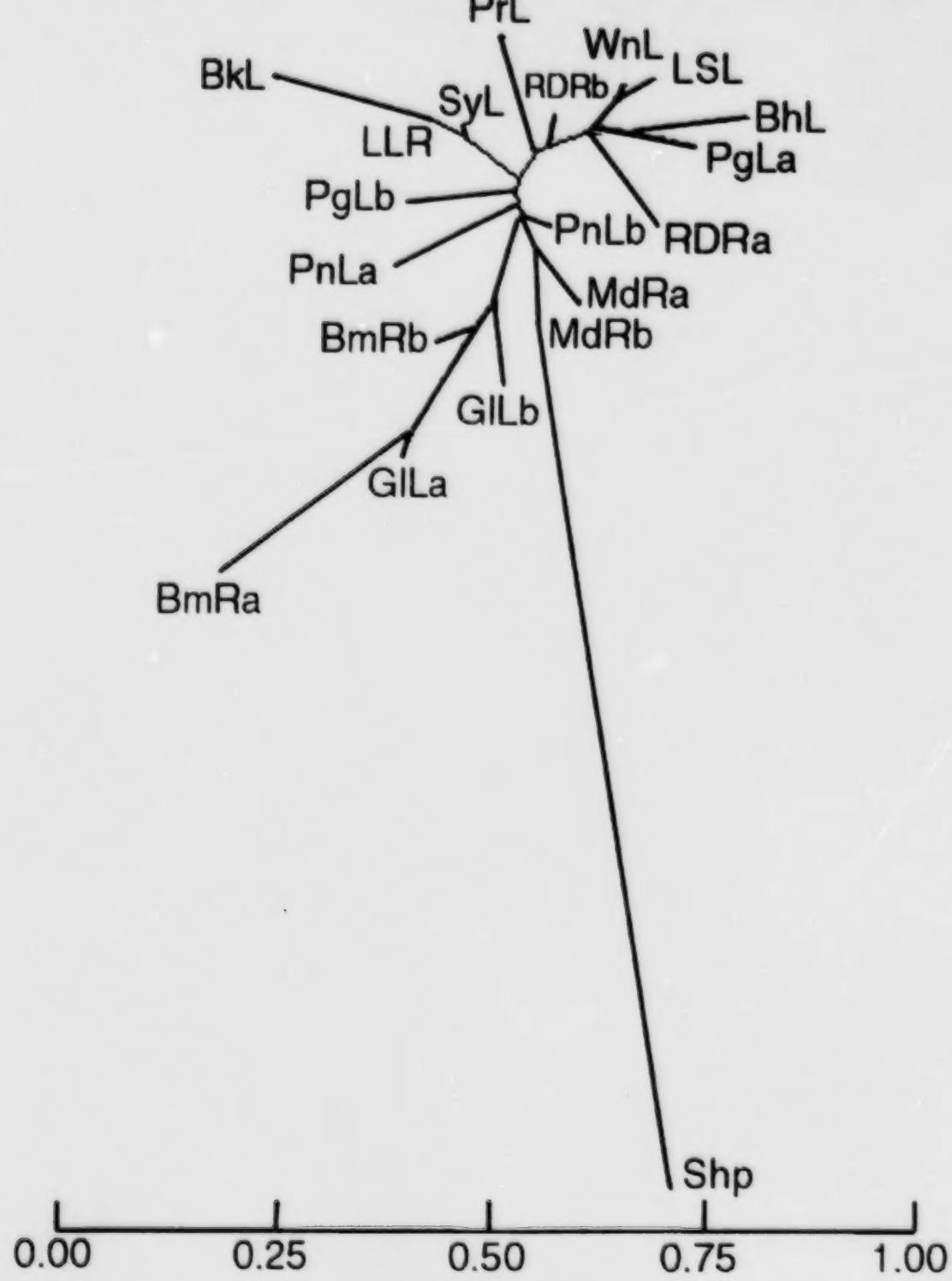


Figure 3. FITCH tree based on Cavalli-Sforza's genetic distance values. All samples were walleye (*Stizostedion vitreum*) except those from the Sheep River (Shp) which were bull trout (*Salvelinus confluentus*). Lower case a / b divide populations into groups thought to be composed of mixed (may contain stocked or non-stocked) fish (a) and non-stocked fish (b). Numbers indicate A distance ruler is provided at the base of the figure.

Lake, Lesser Slave Lake, Winefred Lake and Primrose Lake were grouped together by the KITSCH algorithm. Native fish from the Red Deer River also were placed in this group. In contrast, fish from Lac La Ronge, Saskatchewan were not included in this group.

In general genetic distances between bull trout and walleye averaged 1.39 ± 0.241 and ranged from 1.02 to 1.89 in the samples examined (Table 5). In contrast, genetic distances among all non-stocked walleye (including all "b" samples as well as those from Lac La Ronge, Buck, Primrose, Winefred, Lesser Slave and Bistcho lakes) examined averaged 0.37 ± 0.16, but ranged from 0.09 (c.v. walleye from Lesser Slave Lake and Winefred Lake) to 1.02 (c.v. walleye from Bistcho Lake and Buck Lake), while those of walleye identified as mixed averaged 0.49 ± 0.20 (including all "a" samples plus those from Sylvan Lake which originally was stocked from Lac La Ronge) and ranged from 0.22 (c.v. the mixed walleye group from Sylvan Lake with those from the Medicine River) to 0.98 (c.v. the mixed walleye group from the Blindman River with those from the mixed group from the Red Deer River (Appendix 2)). These averages indicate that some survival of stocked walleye has occurred resulting in higher levels of genetic diversity in mixed walleye populations.

3.3 Genetic Distance Analysis for Individual Study Regions

3.3.1 Pigeon Lake

Walleye are thought to have been extirpated from Pigeon Lake in the 1960's. Walleye fingerlings were stocked into Pigeon Lake from eggs collected from Winefred Lake in 1979, 1980, 1982, 1983 and 1984 to re-establish the population. Pigeon Lake (PgLa) walleye from year-classes that may contain stocked fish introduced from Winefred Lake exhibited a genetic distance (Table 5) of 0.24 relative to native Winefred Lake (WnL) samples and, a genetic distance of 0.30 relative to other walleye from Pigeon Lake (PgLb). In contrast, walleye native to Pigeon Lake had a genetic distance of 0.37 relative to walleye from Winefred Lake (Table 5). Examination of KITSCH (Fig 2) and FITCH (Fig 3) plots of this data show that walleye from the mixed group from Pigeon Lake (PgLa) have genotypes most similar

to those of walleye from Bistcho Lake, but within the same grouping as, their stocking source, walleye from Winefred Lake.

When samples from Pigeon Lake were collected and aged, walleye from a 1981 year-class were identified. The presence of a 1981-year class means that either the native walleye population in Pigeon Lake had not been extirpated or fish stocked in 1979 spawned in 1981 at an age of 2 years. In Alberta, most female walleye mature at age six years or older (Nelson and Paetz 1992). A spawning survey in 1993 found that the youngest mature female walleye in Pigeon Lake were five years old (Boag and Jacobsen 1993). Although the growth rate of walleye in Pigeon Lake is high in comparison to many Alberta lakes, it is doubtful that Pigeon Lake females could mature in only two years. KITSCH (Figure 2) and FITCH (Figure 3) plots of the data (Table 5) show that walleye from the 1981 year-class (PgLb) had genotypes most similar to other walleye from central Alberta. This suggests that the PgLb samples are walleye from a remnant population, native to Pigeon Lake. This also suggests that, since 1985, most of the walleye recruited into the walleye population of Pigeon Lake have a genotype more similar to Winefred Lake walleye than to the walleye native to Pigeon Lake.

3.3.2 Pine Lake

Pine Lake was stocked with eggs from Lac La Ronge in 1960, 1962 and 1963 and with eggs from an unknown Alberta lake in 1961. The eggs from Alberta, however, were reported to be of low quality and very few were thought to be viable (Hunt 1972). Further stocking of Pine Lake occurred in 1988 with walleye from Lesser Slave, Primrose and/or Bistcho Lake (Appendix 2).

Walleye originally stocked into Pine Lake (PnLb) exhibit a genetic distance of 0.22 (Table 5) relative to fish native to Lac La Ronge (LLR), indicating that these fish still are closely related. In contrast, the mixed walleye group from Pine Lake (PnLa), which may contain stocked fish from Lesser Slave (LSL), Primrose (PrL) and Bistcho lakes (BhL) exhibit a genetic distance of 0.20 relative to the original Pine Lake (PnLb) sample and, genetic distances of 0.39, 0.37, 0.49 and 0.42 relative to native

fish surveyed from Lac La Ronge (LLR), Lesser Slave (LSL), Primrose (PrL) and Bistcho lakes (BhL). Since the genetic distance between the mixed (PnLa) and non-stocked (PnLb) groups is much smaller than between the mixed group (PnLa) and the stocking sources used in 1988 (Lesser Slave (LSL), Primrose (PrL) and Bistcho lakes (BhL)), it appears that the mixed group contains mainly resident fish from Pine Lake and few stocked fish. A survey in 1989, found the 1988 year-class (age 1) was the most abundant age-class making up 46% of the walleye sampled, resulting in a very skewed age-class distribution (Buchwald, 1991). Large numbers of age 1 walleye are not common in most surveys and the large numbers caught in 1989 were attributed to the 1988 stocking of walleye fingerlings (Buchwald, 1991). Sampling in 1994, found the 1988 year-class remained abundant at 24% of the sample, but was no longer the most abundant age-class and the age-class distribution was no longer skewed (Buchwald, 1998). Although, there appeared initially to be high survival of the 1988 stocked fish, the fish sampled in 1994 (PnLa, Appendix 1) appear to be more closely related to the non-stocked fish (PnLb) than to the stocking sources used in 1988 (Lesser Slave (LSL), Primrose (PrL) and Bistcho lakes (BhL)). This indicates that survival of the stocked fish was poor.

Examination of KITSCH (Fig. 2) and FITCH (Fig. 3) plots suggest that walleye populations from Pine Lake (PnLb) and Lac La Ronge (LLR) may belong to genetically separate groups. This suggests that there has been selection in Pine Lake for certain genotypes since walleye from Lac La Ronge were introduced into Pine Lake in the early 1960s.

3.3.3 Sylvan Lake

Sylvan Lake was stocked with eggs from Lac La Ronge in 1960, 1962 and 1963 and with eggs from an unknown Alberta lake in 1961 using the same source that was used to stock Pine Lake. As indicated above, eggs introduced into Sylvan Lake from the unknown Alberta source were reported to be of low quality and very few are thought to have survived (Hunt 1972).

The genetic distance (Table 5) of walleye from Sylvan Lake relative to Lac La Ronge was 0.07. This low genetic distance value indicates that the composition of the population of walleye found in Sylvan Lake is genetically similar, if not identical to that found in Lac La Ronge. KITSCH (Fig 2) and

FITCH (Fig 3) transformations of the data visually illustrate this finding and show that population data for walleye from both Sylvan Lake and Lac La Ronge repeatedly segregate together. The bootstrap value, measure of confidence, for the Sylvan Lake/Lac La Ronge branch is 87% (Fig. 2) and genetically is well supported; i.e. this group of fish genotypes repeatedly segregates from all other walleye examined 87 % of the time in the analysis. In contrast the bull trout outgroup (Shp) has a bootstrap value of 100%.

Although the walleye population in Sylvan Lake is self-sustaining, recruitment in Sylvan Lake appears to be limited. Previous studies (Pattenden 1994, 1995) have shown that 13% of the mature females in Sylvan Lake resorb their eggs instead of spawning, and that the remainder spawn over vegetation instead of the normally preferred rocky substrate, which is readily available in Sylvan Lake. This suggests that the current stock of walleye in Sylvan Lake (originally from Lac La Ronge) may not be suited to the environment that they have been introduced to. No evidence of adaptation through genetic drift of the population was detected.

The genetic distance (Table 5) of fish from Sylvan Lake (Syl) relative to original stocks from Pine Lake (PnLb) was 0.22. As indicated above, the population of walleye from Pine Lake appears to exhibit some genetic drift relative to native fish from Lac La Ronge. This drift may reflect adaptation of these fish to Pine Lake. Examination of KITSCH (Fig 2) and FITCH (Fig 3) plots suggests that Sylvan Lake (Syl) and Pine Lake (PnLb) walleye belong to separate populations. Both groupings appear distinct from other walleye sampled in northern Alberta and Saskatchewan.

3.3.4 Red Deer, Little Red Deer, Medicine, and Blindman Rivers

The Red Deer (RDR), Little Red Deer, Medicine (MdR), and Blindman (BmR) rivers are part of the same drainage system. Comparison of walleye native to these rivers (Table 5) indicates that each river in the drainage may house a unique walleye population; i.e. RDRb c.v. MdRb is 0.34; RDRb c.v. BmRb is 0.29 and MdRb c.v. BmRb is 0.43. Examination of KITSCH (Fig 2) and FITCH (Fig 3) plots of the data support this conclusion, showing that each population of fish sampled may belong to a separate group or arm on the plots. This suggests that these fish are part of a dynamic system in which

groups of walleye show preference for a home spawning ground or territory. This spawning philopatry has been recognized in salmon for some time and more recently has been noted in walleye (Stepien and Farber, 1998).

Genetic distances between each of the groups of native walleye obtained from the Red Deer drainage are smaller than those obtained between mixed groups of fish taken from rivers in the region which appear to contain stocked fish that escaped from Gleniffer Lake; i.e. RDRa c.v. MdRa is 0.47; RDRa c.v. BmRa is 0.98; and MdRa c.v. BmRa is 0.64. Samples collected from the Red Deer River were obtained from km 110 to km 425 (river km were measured starting at zero at the Saskatchewan border). The confluence of the Red Deer River and the Blindman River is at km 492; the confluence with the Medicine River is at km 565.5. These genetic distances reflect that the mixed groups of fish sampled, not only were obtained from sites geographically and to some degree reproductively separate from one another, but, also suggest that fish native to the lower Red Deer (RDRb), Medicine/Little Red Deer (MdRb), and Blindman (BmRb) rivers mix and breed together under some circumstances. Genetic distance values for the mixed walleye groups in this region are discussed in more depth below.

The Little Red Deer, Medicine, and Blindman rivers all flow into the Red Deer River downstream of Gleniffer Lake, a reservoir above Dickson Dam on the Red Deer River. In 1988, 1989 and 1990 walleye were stocked into Gleniffer Lake from Lesser Slave and Primrose lakes. Walleye stocked into Gleniffer Lake appear to be present in samples from the Red Deer (RDRa), Medicine/Little Red Deer (MdRa), and Blindman rivers (BmRa).

Both native (RDRa) and mixed (RDRb) populations of walleye found in the Red Deer River had genotypes similar to those found in northern Alberta and Saskatchewan (Table 5); i.e. the genetic distance for RDRb c.v. LSL was 0.20; for RDRa c.v. LSL was 0.21; while RDRb c.v. PrL was 0.20; and RDRa c.v. PrL was 0.31. KITSCH (Fig. 2) and FITCH (Fig. 3) plots of the data also show that walleye from the Red Deer River are grouped with fish from northern Alberta and Saskatchewan; i.e. fish from the Red Deer River were grouped with fish from Primrose, Lesser Slave, Winefred and Bistcho lakes.

Comparison of native walleye (Table 5) from the Medicine /Little Red Deer rivers (MdRb) with the mixed walleye group from the Medicine /Little Red Deer rivers (MdRa) produced a genetic distance

value of 0.10. Both KITSCH (Fig. 2) and FITCH (Fig. 3) plots show that the two groups of fish are genetically similar if not identical. Comparison of the mixed walleye group from the Medicine /Little Red Deer rivers (MdRa) with native fish from both Lesser Slave Lake (LSL) and Primrose Lake (PrL) produced larger genetic distance values of 0.36 and 0.34 respectively. Both KITSCH (Fig. 2) and FITCH (Fig. 3) plots also suggest that the MdRa walleye are genetically distinct from walleye obtained from both Lesser Slave Lake (LSL) and Primrose Lake (PrL). This suggests that very few or none of the stocked fish from Gleniffer Lake had mixed with the walleye in the Medicine River.

Comparison of native walleye (Table 5) from the Blindman River (BmRb) with the mixed group from the Blindman River (BmRa) produced a genetic distance value of 0.40. Comparison of fish from the Blindman River mixed group (BmRa) with fish from both Lesser Slave Lake (LSL) and Primrose Lake (PrL) produced genetic distance values of 0.90 and 0.89 respectively. Examination of the data on KITSCH (Fig. 2) and FITCH (Fig. 3) plots suggests that each of these groups is genetically different. It appears that the Blindman River mixed group contains both native fish and stocked fish from Gleniffer Lake.

3.3.5 Gull Lake

Gull Lake (GlL) and the Blindman River (BmR) both are part of the Blindman/Red Deer River Drainage System. However, there has been no outflow from Gull Lake into the Blindman River since early this century. Gull Lake has a native walleye population (GlLb), but it was stocked in 1986, 1987, 1988 and 1989 with walleye from Lesser Slave (LSL), Primrose (PrL) and Bistcho lakes (BhL). Comparison of walleye native to Gull Lake (GlLb) with fish native to the Blindman River (BmRb) produced a genetic distance value of 0.41. Examination of the FITCH tree (Fig 2) produced from the data indicates these fish are on the same arm of the tree and consequently, genetically may be close to one another. We note that the genetic distance value between these fish is similar to those obtained for other fish native to the Red Deer River drainage system as shown above (Table 5); i.e. the genetic distance of native fish from Gull Lake (GlLb) c.v. native fish from the Medicine River (MdRb) was 0.28 while that of native fish from Gull Lake (GlLb) c.v. native fish from the Red Deer River (RDRb) was

0.35. That the genetic distance value is slightly larger than expected for fish from the same drainage may result from segregation of Gull Lake from the Blindman River since early this century.

Comparison of fish native to Gull Lake (GlLb) with the mixed group from Gull Lake (GlLa), which may contain fish from Lesser Slave (LSL), Primrose (PrL) and Bistcho lakes (BhL) produced a genetic distance value of 0.26. Comparison of the mixed group from Gull Lake (GlLa) with fish native to Lesser Slave (LSL), Primrose (PrL) and Bistcho lakes (BhL) resulted in genetic distance values of 0.74, 0.63, and 0.69 respectively. This suggests that stocked fish from Lesser Slave (LSL), Primrose (PrL) and Bistcho lakes (BhL) made up a low proportion of the mixed fish group and that the mixed fish group was largely made up of native fish. We note that no common genotypes (Table 2) could be identified among the stocked fish (GlLa) and the stocking sources. Consequently, it was not possible to determine the original source of the surviving stocked fish in Gull Lake.

3.3.6 Buck Lake

Buck Lake (BkL) contains one of the more successful walleye populations in Alberta and could provide a source of fish for stocking in the future. The walleye population from Buck Lake on average exhibited a genetic distance of 0.43 ± 0.17 relative to other "non-stocked" walleye in the Parkland Region (Table 5); i.e. as compared to non-stocked walleye from Pigeon Lake (PgLb), Medicine River (MdRb), Blindman River (BmRb), Sylvan Lake (SyL), Gull Lake (GlL), Pine Lake (PnL) and the Red Deer River (RDRb). When walleye from Buck Lake were compared with populations of fish from lakes in northern Alberta and Saskatchewan the average genetic distance was 0.60 ± 0.31. Examination of phenograms generated using KITSCH (Fig. 2) and FITCH (Fig. 3) algorithms suggests that fish from Buck Lake may be most closely related to fish from Lac La Ronge and Sylvan Lake.

3.3.7 Lesser Slave, Winefred, Bistcho and Primrose Lakes

Walleye from Lesser Slave and Winefred lakes appear closely related genetically; i.e. fish from Lesser Slave Lake c.v. Winefred Lake exhibited a genetic distance of 0.09 (Table 5). Fish from these lakes also were paired in a KITSCH tree (Fig. 2) with a bootstrap value of 69%, indicating strong

support for the association. Lesser Slave and Winefred lakes are both in the Athabasca drainage and are located at latitude 55.5° North. Although, they are separated by several hundred kilometers of river there appears to be a continual exchange of genetic material within the drainage or adaptive pressures are similar in both water bodies.

When fish from Lesser Slave Lake and Winefred Lake were compared with those from either Bistcho or Primrose lakes the genetic distances ranged from 0.20 to 0.32 (Table 5). Fish from Bistcho and Primrose lakes were separated by a genetic distance of 0.41. Walleye from each of these lakes appear to be part of the same group in both KITSCH (Fig. 2) and FITCH (Fig. 3) plots. Bootstrap values calculated for the KITSCH plot also indicate support for separation of these fish as an independent group. Regional geographic variation in walleye stocks has been observed for mitochondrial DNA markers (Billington et. al., 1992). In their study Billington et al. (1992) found that samples from Bistcho, Lesser Slave, and Primrose lakes all had a common mitochondrial DNA haplotype which was geographically situated within the northwest of Canada and the United States but, not found in central or eastern regions of the continent. Our studies support those of Billington et al. (1992) which indicate that fish from Bistcho, Lesser Slave, and Primrose lakes fall into a common group but, also indicate that additional groups of genetically distinct walleye exist within the provinces of Alberta and Saskatchewan.

3.3.8 Lac La Ronge

As indicated above the genetic distance (Table 5) of walleye from Sylvan Lake relative to Lac La Ronge was 0.07 suggesting that the composition of the population of walleye found in Sylvan Lake is genetically similar, if not identical to that found in Lac La Ronge. This relationship is a function of the stocking program which introduced fish from Lac La Ronge into Sylvan Lake.

Conclusions

These studies strongly suggest:

1. that distinct populations of walleye exist within different regions of Alberta and Saskatchewan;
2. that populations of walleye found in different regions of Alberta and Saskatchewan possess genotypes which appear regionally adapted;
3. that there has been survival of stocked walleye in water bodies and;
4. that in cases where there was an existing walleye population (ie. Pigeon Lake) naturalized fish now are breeding with fish native to the region.

Specifically, our study indicates that:

1. There was a small remnant native walleye population still remaining in Pigeon Lake when it was stocked with walleye from 1979 to 1984. The walleye recruited in Pigeon Lake since 1985 have genotypes more similar to Winefred Lake walleye than to the native Pigeon Lake stock.
2. Walleye from Lac La Ronge and Sylvan Lake are genetically very similar and appear distinct from other walleye groups. There is no evidence for selection on the walleye population introduced to Sylvan Lake from Lac La Ronge. In contrast, walleye recovered from Pine Lake, that are offspring of fish introduced from Lac La Ronge, are genetically different from the source stock, suggesting that these fish were subjected to selective pressures. Walleye from Pine Lake appear to belong to a genetically separate group, different from walleye found in Lac La Ronge and Sylvan Lake.
3. Some of the walleye stocked into Pine Lake in 1988 appear to have survived; however, fish sampled in 1994 that were six years old appear to be mainly non-stocked fish.
4. Walleye stocks from the lower Red Deer, Medicine, and Blindman rivers are genetically different indicating that different stocks may be present; however, the amount of difference between the groups suggests that there has been some exchange of genetic material between the groups.

5. There appears to be some evidence that walleye stocked in Gleniffer Lake moved below Dickson Dam. The stocked fish appear to have a higher presence in the Red Deer River than in either the Blindman or the Medicine rivers.

Acknowledgments

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Appendix 1. Sample information reported on fin envelopes provided with each sample from Pine Lake, Buck Lake, Sylvan Lake, Medicine River, Gull Lake, Blindman River and Lake, Red Deer River, Little Red Deer River, Pigeon Lake, Lac La Ronge, Primrose Lake, Winefred Lake, Bistcho Lake, Lesser Slave Lake, and the Sheep River. All samples were walleye *(Stizostedion vitreum)*, except those from the Sheep River which were bull trout *(Salvelinus confluentus)*.

Sample	Species	Sex	Age	Weight (g)	Length (cm)	Water	Location
W1	Wall	NR	14	1535	54.1	Pine Lake	NR
W23	Wall	NR	7	920	44.9	Pine Lake	NR
W24	Wall	NR	6	580	37.8	Pine Lake	NR
W25	Wall	NR	5	715	39.6	Pine Lake	NR
W26	Wall	NR	6	1305	49.0	Pine Lake	NR
W27	Wall	NR	6	1155	46.3	Pine Lake	NR
W28	Wall	NR	16	2905	61.5	Pine Lake	NR
W29	Wall	NR	5	715	40.9	Pine Lake	NR
W30	Wall	NR	6	900	43.9	Pine Lake	NR
W31	Wall	NR	10	2485	59.1	Pine Lake	NR
W201	Wall	NR	6	1285	47.8	Pine Lake	NR
W202	Wall	NR	6	780	41.8	Pine Lake	NR
W203	Wall	NR	6	1120	45.1	Pine Lake	NR
W204	Wall	NR	6	900	43.5	Pine Lake	NR
W205	Wall	NR	6	870	43.4	Pine Lake	NR
W206	Wall	NR	6	1150	46.4	Pine Lake	NR
W2	Wall	M	5	570	39.0	Buck Lake	WWC
W5	Wall	NR	6	815	42.2	Buck Lake	Creel
W6	Wall	M	7	610	40.3	Buck Lake	Creel
W7	Wall	M	6	715	41.7	Buck Lake	Creel
W8	Wall	M	7	585	38.8	Buck Lake	Creel
W9	Wall	M	6	665	39.4	Buck Lake	Creel
W10	Wall	F	7	835	42.8	Buck Lake	Creel
W11	Wall	M	5	540	38.0	Buck Lake	NR
W21	Wall	F	7	970	44.9	Buck Lake	Creel
W22	Wall	M	5	495	36.7	Buck Lake	Creel
W3	Wall	NR	3	356	31.8	Sylvan Lake	ES19
W12	Wall	NR	7	903	44.5	Sylvan Lake	ES11
W13	Wall	NR	8	1240	49.7	Sylvan Lake	ES11
W14	Wall	NR	8	1444	51.0	Sylvan Lake	ES11
W15	Wall	NR	6	1419	47.8	Sylvan Lake	NR
W16	Wall	NR	NR	1059	46.0	Sylvan Lake	ES11
W17	Wall	NR	6	1061	46.8	Sylvan Lake	ES11
W18	Wall	NR	5	1047	45.8	Sylvan Lake	ES11
W19	Wall	NR	6	1346	49.0	Sylvan Lake	ES11
W20	Wall	NR	NR	1170	48.7	Sylvan Lake	ES11
W4	Wall	NR	14	4024	72.2	Medicine River	km 0.5
W32	Wall	NR	13	3287	65.9	Medicine River	km 3.6
W33	Wall	NR	9	2495	60.3	Medicine River	km 2.8
W34	Wall	NR	10	2382	61.8	Medicine River	km 3.6
W35	Wall	NR	4	671	41.1	Medicine River	km 2.8
W36	Wall	NR	5	909	44.4	Medicine River	km 2.8
W37	Wall	NR	12	2357	64.0	Medicine River	km 0.8
W38	Wall	NR	5	1224	50.3	Medicine River	Trap
W39	Wall	NR	9	2295	61.7	Medicine River	km 0.8
W40	Wall	NR	5	1116	49.0	Medicine River	km 3.0
W186	Wall	NR	4	NR	NR	Medicine River	NR
W187	Wall	NR	4	NR	NR	Medicine River	NR
W188	Wall	NR	3	368	33.2	Medicine River	Upper Trap
W189	Wall	F	10	3083	66.0	Medicine River	NR
W190	Wall	NR	4	640	39.4	Medicine River	NR
W191	Wall	F	14	4008	74.8	Medicine River	NR
W192	Wall	F	13	2956	66.6	Medicine River	NR
W193	Wall	F	9	2192	59.8	Medicine River	NR
W41	Wall	F	5	830	41.7	Gull Lake	Creel-Wilsons
W42	Wall	M	5	870	43.5	Gull Lake	Creel-Aspen
W43	Wall	F	9	1650	52.5	Gull Lake	Creel-Aspen
W44	Wall	F	4	570	38.8	Gull Lake	Creel-Sunset
W45	Wall	F	10	1150	49.1	Gull Lake	Creel-Aspen

Sample	Species	Sex	Age	Weight (g)	Length (cm)	Water	Location
W46	Wall	M	4	810	40.3	Gull Lake	Creel-Aspen
W47	Wall	F	11	1520	56.3	Gull Lake	Creel-Aspen
W48	Wall	NR	10	1310	56.0	Gull Lake	Creel-Aspen
W49	Wall	NR	5	730	40.1	Gull Lake	Creel-Wilson
W50	Wall	F	4	735	39.4	Gull Lake	Creel-Wilson
W194	Wall	NR	NR	NR	NR	Gull Lake	NR
W195	Wall	NR	NR	NR	NR	Gull Lake	NR
W196	Wall	NR	NR	NR	NR	Gull Lake	NR
W197	Wall	NR	NR	NR	NR	Gull Lake	NR
W198	Wall	NR	NR	NR	NR	Gull Lake	NR
W199	Wall	NR	NR	NR	NR	Gull Lake	NR
W200	Wall	NR	NR	NR	NR	Gull Lake	NR
W51	Wall	NR	5	1258	47.9	Blindman River	km 2.0
W25	Wall	NR	4	755	40.3	Blindman River	Trap
W53	Wall	NR	5	1110	46.2	Blindman River	Trap
W54	Wall	NR	5	607	41.1	Blindman River	NR
W55	Wall	NR	5	1113	46.7	Blindman River	km 15.9
W56	Wall	F	8	2205	62.6	Blindman River	Trap
W57	Wall	NR	9	1960	58.9	Blindman River	km 0.0
W58	Wall	NR	5	665	14.5	Blindman River	Trap
W59	Wall	NR	4	650	42.2	Blindman River	Trap
W60	Wall	NR	6	850	44.1	Blindman River	Trap
W179	Wall	NR	5	760	40.7	Blindman River	Mouth
W180	Wall	NR	8	2680	62.6	Blindman River	Mouth
W61	Wall	NR	7	770	42.8	Red Deer River	km 425
W62	Wall	NR	2	270	30.4	Red Deer River	km 425
W63	Wall	NR	4	740	39.4	Red Deer River	km 415
W64	Wall	NR	3	370	32.7	Red Deer River	km 410
W65	Wall	NR	3	560	38.8	Red Deer River	km 375
W66	Wall	NR	3	310	32.1	Red Deer River	km 130
W67	Wall	NR	4	570	38.0	Red Deer River	km 115
W68	Wall	NR	4	500	37.5	Red Deer River	km 115
W69	Wall	NR	4	410	34.5	Red Deer River	km 115
W70	Wall	NR	6	770	43.5	Red Deer River	km 110
W71	Wall	NR	6	1201	51.2	Little Red Deer River	km 0.0
W72	Wall	NR	9	3189	65.9	Little Red Deer River	km 0.0
W207	Wall	NR	10	4010	69.1	Red Deer River	km 325
W208	Wall	NR	9	2680	63.7	Red Deer River	km 185
W209	Wall	NR	6	250	31.1	Red Deer River	km 170
W210	Wall	NR	2	100	21.5	Red Deer River	km 175
W211	Wall	NR	2	70	21.1	Red Deer River	km 185
W212	Wall	NR	2	70	20.5	Red Deer River	km 190
W73	Wall	NR	7	2580	60.5	Pigeon Lake	Tide Creek
W74	Wall	M	7	1750	53.2	Pigeon Lake	Tide Creek
W75	Wall	NR	9	NR	66.0	Pigeon Lake	WWC
W76	Wall	NR	10	3856	67.3	Pigeon Lake	WWC
W77	Wall	NR	10	4479	72.4	Pigeon Lake	WWC
W78	Wall	NR	10	3742	68.6	Pigeon Lake	WWC
W79	Wall	NR	10	NR	63.5	Pigeon Lake	WWC
W80	Wall	NR	10	3600	63.5	Pigeon Lake	WWC
W81	Wall	NR	3	1559	45.7	Pigeon Lake	WWC
W82	Wall	NR	3	1474	45.7	Pigeon Lake	WWC
W181	Wall	NR	4	1200	45.0	Pigeon Lake	Grandview
W182	Wall	NR	4	1700	49.5	Pigeon Lake	Mulhurst
W183	Wall	NR	4	1580	51.5	Pigeon Lake	Grandview
W184	Wall	NR	4	1340	47.0	Pigeon Lake	Ma Ma O
W185	Wall	NR	4	1650	51.0	Pigeon Lake	Grandview
W213	Wall	NR	4	1250	45.5	Pigeon Lake	Grandview
W83	Wall	M	NR	1525	48.0	L. L. Ronge	NR
W84	Wall	M	NR	1200	46.0	L. L. Ronge	NR
W85	Wall	NR	NR	110	21.0	L. L. Ronge	NR
W86	Wall	M	NR	900	42.0	L. L. Ronge	NR
W87	Wall	F	NR	1225	46.0	L. L. Ronge	NR
W88	Wall	M	NR	1450	47.0	L. L. Ronge	NR
W89	Wall	M	NR	925	43.0	L. L. Ronge	NR
W90	Wall	M	NR	1050	43.0	L. L. Ronge	NR
W91	Wall	M	NR	1450	48.0	L. L. Ronge	NR
W92	Wall	M	NR	1150	47.0	L. L. Ronge	NR
W93	Wall	M	NR	1250	47.0	L. L. Ronge	NR
W94	Wall	M	NR	1100	45.0	L. L. Ronge	NR
W95	Wall	M	NR	1500	50.0	L. L. Ronge	NR
W96	Wall	F	NR	1125	43.0	L. L. Ronge	NR

Sample	Species	Sex	Age	Weight (g)	Length (cm)	Water	Location
W97	Wall	M	NR	550	37.0	L. L. Ronge	NR
W98	Wall	F	NR	1175	47.0	L. L. Ronge	NR
W99	Wall	M	NR	1400	47.0	L. L. Ronge	NR
W100	Wall	F	NR	1000	45.0	L. L. Ronge	NR
W101	Wall	F	NR	725	40.0	L. L. Ronge	NR
W102	Wall	M	NR	800	41.0	L. L. Ronge	NR
W103	Wall	M	NR	1300	49.0	L. L. Ronge	NR
W104	Wall	M	6	1300	41.8	Primrose Lake	Brett Creek
W105	Wall	M	13	1800	52.2	Primrose Lake	Brett Creek
W106	Wall	F	7	1840	50.3	Primrose Lake	Brett Creek
W107	Wall	M	6	1380	42.4	Primrose Lake	Brett Creek
W108	Wall	F	18	3250	69.5	Primrose Lake	Brett Creek
W109	Wall	F	9	1600	51.8	Primrose Lake	Brett Creek
W110	Wall	F	15	3400	63.6	Primrose Lake	Brett Creek
W111	Wall	F	8	1880	49.6	Primrose Lake	Brett Creek
W112	Wall	F	15	3100	62.4	Primrose Lake	Brett Creek
W113	Wall	F	18	3650	67.0	Primrose Lake	Brett Creek
W114	Wall	F	8	1800	50.5	Primrose Lake	Brett Creek
W115	Wall	F	10	1600	51.5	Primrose Lake	Brett Creek
W116	Wall	F	12	2150	59.1	Primrose Lake	Brett Creek
W117	Wall	F	11	2980	60.4	Primrose Lake	Brett Creek
W118	Wall	F	15	2400	58.2	Primrose Lake	Brett Creek
W119	Wall	NR	10	2200	57.2	Winnefred Lake	NR
W120	Wall	NR	10	1920	56.5	Winnefred Lake	NR
W121	Wall	NR	8	1020	46.5	Winnefred Lake	NR
W122	Wall	NR	9	1420	49.8	Winnefred Lake	NR
W123	Wall	NR	187	2000	56.9	Winnefred Lake	NR
W124	Wall	NR	10	2200	58.1	Winnefred Lake	NR
W125	Wall	NR	10	1900	56.9	Winnefred Lake	NR
W126	Wall	NR	7	1260	49.0	Winnefred Lake	NR
W127	Wall	NR	11	1600	52.4	Winnefred Lake	NR
W128	Wall	NR	9	1500	50.9	Winnefred Lake	NR
W129	Wall	NR	10	1980	56.7	Winnefred Lake	NR
W130	Wall	NR	8	1120	46.8	Winnefred Lake	NR
W131	Wall	NR	10	1920	56.5	Winnefred Lake	NR
W132	Wall	NR	11	2780	55.6	Winnefred Lake	NR
W133	Wall	NR	12	2150	59.6	Winnefred Lake	NR
W134	Wall	NR	16	2200	58.1	Winnefred Lake	NR
W135	Wall	NR	8	1100	46.9	Winnefred Lake	NR
W136	Wall	NR	10	1680	52.8	Winnefred Lake	NR
W137	Wall	NR	8	1320	48.4	Winnefred Lake	NR
W138	Wall	NR	9	1420	50.0	Winnefred Lake	NR
W139	Wall	M	NR	1775	48.9	Bistcho Lake	NW Kirknoss Crey
W140	Wall	F	NR	2100	53.6	Bistcho Lake	NW Kirknoss Crey
W141	Wall	F	NR	2425	56.1	Bistcho Lake	NW Kirknoss Crey
W142	Wall	F	NR	2550	58.0	Bistcho Lake	NW Kirknoss Crey
W143	Wall	M	NR	1550	49.3	Bistcho Lake	NW Kirknoss Crey
W144	Wall	F	NR	2150	55.6	Bistcho Lake	West Jackfish Point
W145	Wall	F	NR	1125	49.0	Bistcho Lake	West Jackfish Point
W146	Wall	F	NR	2550	57.8	Bistcho Lake	NR
W147	Wall	F	NR	1325	48.6	Bistcho Lake	NR
W148	Wall	F	NR	2075	52.2	Bistcho Lake	East of Rochos Camp
W149	Wall	F	NR	1200	45.9	Bistcho Lake	East of Rochos Camp
W150	Wall	M	NR	1325	47.0	Bistcho Lake	East of Rochos Camp
W151	Wall	F	NR	1075	46.7	Bistcho Lake	East of Rochos Camp
W152	Wall	F	NR	950	44.5	Bistcho Lake	East of Rochos Camp
W153	Wall	M	NR	1525	49.8	Bistcho Lake	East of Rochos Camp
W154	Wall	F	NR	2400	56.5	Bistcho Lake	East of Rochos Camp
W155	Wall	M	NR	1175	43.3	Bistcho Lake	N Shore
W156	Wall	M	NR	1825	51.4	Bistcho Lake	N Shore Dog Island
W157	Wall	M	NR	1825	51.6	Bistcho Lake	N Shore Dog Island
W158	Wall	F	NR	2550	58.0	Bistcho Lake	N Shore Dog Island
W159	Wall	NR	NR	NR	NR	Lesser Slave Lake	NR
W160	Wall	NR	NR	NR	NR	Lesser Slave Lake	NR
W161	Wall	NR	NR	NR	NR	Lesser Slave Lake	NR
W162	Wall	NR	NR	NR	NR	Lesser Slave Lake	NR
W163	Wall	NR	NR	NR	NR	Lesser Slave Lake	NR
W164	Wall	NR	NR	NR	NR	Lesser Slave Lake	NR
W165	Wall	NR	NR	NR	NR	Lesser Slave Lake	NR
W166	Wall	NR	NR	NR	NR	Lesser Slave Lake	NR
W167	Wall	NR	NR	NR	NR	Lesser Slave Lake	NR
W168	Wall	NR	NR	NR	NR	Lesser Slave Lake	NR

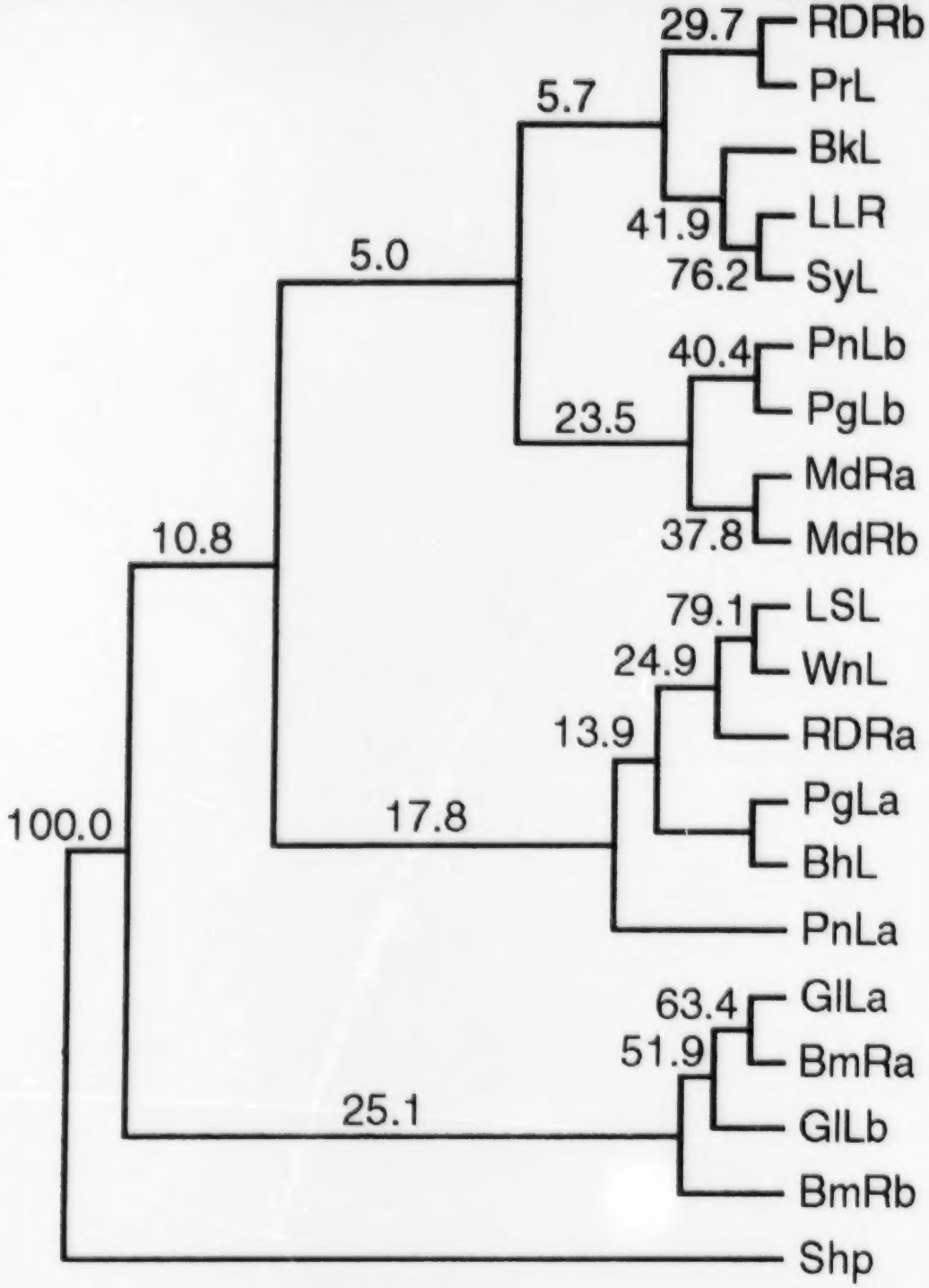
Sample	Species	Sex	Age	Weight (g)	Length (cm)	Water	Location
W169	Wall	NR	NR	NR	NR	Lesser Slave Lake	NR
W170	Wall	NR	NR	NR	NR	Lesser Slave Lake	NR
W171	Wall	NR	NR	NR	NR	Lesser Slave Lake	NR
W172	Wall	NR	NR	NR	NR	Lesser Slave Lake	NR
W173	Wall	NR	NR	NR	NR	Lesser Slave Lake	NR
W174	Wall	NR	NR	NR	NR	Lesser Slave Lake	NR
W175	Wall	NR	NR	NR	NR	Lesser Slave Lake	NR
W176	Wall	NR	NR	NR	NR	Lesser Slave Lake	NR
W177	Wall	NR	NR	NR	NR	Lesser Slave Lake	NR
W178	Wall	NR	NR	NR	NR	Lesser Slave Lake	NR
Shp1	BLTR	NR	NR	406	34.2	Sheep River	NR
Shp2	BLTR	NR	NR	397	34.1	Sheep River	NR
Shp3	BLTR	NR	NR	285	30.0	Sheep River	NR
Shp4	BLTR	NR	NR	365	32.8	Sheep River	NR
Shp5	BLTR	NR	NR	261	29.7	Sheep River	NR
Shp6	BLTR	NR	NR	369	33.1	Sheep River	NR
Shp7	BLTR	NR	NR	536	37.2	Sheep River	NR
Shp8	BLTR	NR	NR	427	34.0	Sheep River	NR
Shp9	BLTR	NR	NR	134	22.4	Sheep River	NR
Shp10	BLTR	NR	NR	99	21.1	Sheep River	below Black Diamond
Shp11	BLTR	NR	NR	440	35.7	Sheep River	NR
Shp12	BLTR	NR	NR	141	23.8	Sheep River	NR
Shp13	BLTR	NR	NR	348	32.4	Sheep River	NR
Shp15	BLTR	NR	NR	657	39.6	Sheep River	NR
Shp16	BLTR	NR	NR	463	34.9	Sheep River	NR

Appendix 2. Walleye that most likely are stocked fish and their stocking source.

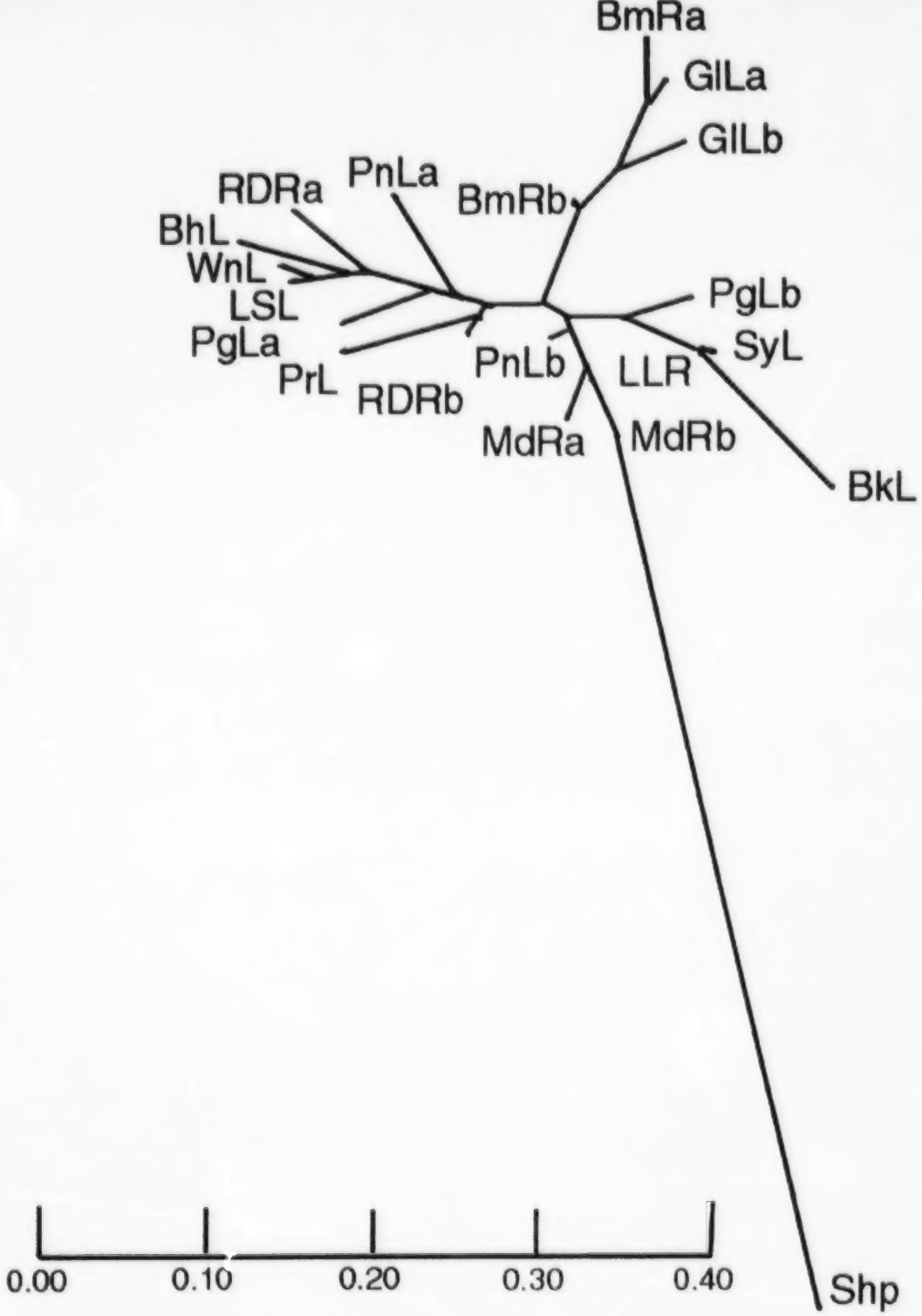
Water Body	Sample Numbers	Stocking Source
Gull Lake	W41, W42, W44, W46, W49, W50	Lesser Slave L, Primrose L, Bistcho L.
Pine Lake	W24, W26, W27, W30, W201, W202, W203, W204, W205, W206	Lesser Slave L, Primrose L, Bistcho L.
Pigeon Lake	W73, W74, W75, W181, W182, W183, W184, W213	Winefred L.
Red Deer River	W62, W64, W65, W210, W211, W212	Lesser Slave L, Primrose L. escaped from Gleniffer L.
Blindman River	W51, W52, W53, W54, W55, W58, W59	Lesser Slave L, Primrose L. escaped from Gleniffer L.
Medicine River	W35, W36, W38, W40, W186, W187, W188, W190	Lesser Slave L, Primrose L. escaped from Gleniffer L.

Appendix 3. Genetic distance values generated with Nei's distance algorithm using PHYLIP version 3.5. All populations were walleye (*Stizostedioon vitreum*) except those from the Sheep River (Shp) which were bull trout (*Salvelinus confluentus*). Lower case a / b divide populations into groups thought to be composed of mixed (may contain stocked or non-stocked) fish (a) and non-stocked fish (b).

	Shp	PnLa	PnLb	BkL	SyL	MdRa	MdRb	GlLa	GlLb	BmRa	BmRb	RDRa	RDRb	PgLa	PgLb	LLR	PrL	WnL	BhL
PnLa	0.5772																		
PnLb	0.5744	0.1025																	
BkL	0.9845	0.3215	0.1595																
SyL	1.1591	0.2048	0.1352	0.1062															
MdRa	0.5025	0.1530	0.0750	0.1989	0.1383														
MdRb	0.4665	0.1146	0.0766	0.1492	0.1505	0.0703													
GlLa	0.5438	0.2489	0.1174	0.3953	0.2678	0.1788	0.1742												
GlLb	0.7055	0.1935	0.1458	0.3200	0.1402	0.1419	0.1826	0.0804											
BmRa	0.8748	0.2729	0.1707	0.5230	0.2494	0.2079	0.2926	0.0564	0.1114										
BmRb	0.6728	0.2076	0.0998	0.3318	0.1580	0.1569	0.1927	0.0923	0.1407	0.0868									
RDRa	0.6394	0.1349	0.1620	0.3114	0.2040	0.2715	0.2226	0.3184	0.2906	0.3675	0.1575								
RDRb	0.7649	0.1515	0.0837	0.1756	0.0893	0.1473	0.2030	0.2295	0.1616	0.2183	0.1065	0.1023							
PgLa	0.6051	0.0997	0.1023	0.4213	0.2024	0.1318	0.1832	0.2099	0.1796	0.1900	0.1193	0.1627	0.1396						
PgLb	0.9005	0.2172	0.0544	0.1363	0.0799	0.0953	0.1346	0.2063	0.1730	0.2179	0.1525	0.2399	0.0915	0.1301					
LLR	1.0343	0.2275	0.1277	0.0642	0.0335	0.1790	0.1313	0.3275	0.2423	0.3800	0.1824	0.1661	0.1124	0.2322	0.0908				
PrL	0.7739	0.2325	0.1772	0.2430	0.1096	0.2001	0.2534	0.3037	0.1548	0.3209	0.1682	0.1286	0.0737	0.1857	0.1507	0.1319			
WnL	0.5809	0.1892	0.1473	0.3053	0.1687	0.1542	0.2308	0.3212	0.2812	0.3013	0.1129	0.0899	0.0874	0.1339	0.1872	0.1719	0.1623		
BhL	0.6152	0.1442	0.1947	0.5212	0.2751	0.2676	0.3299	0.3130	0.2399	0.3039	0.1319	0.1128	0.1306	0.0879	0.2852	0.2831	0.1629	0.1083	
LSL	0.7168	0.1476	0.1638	0.3229	0.1384	0.1904	0.2477	0.3623	0.2500	0.3314	0.1409	0.0858	0.0909	0.1162	0.1984	0.1448	0.1307	0.0286	0.0640



Appendix 4. KITSCH tree based on Nei's genetic distance values. All samples were walleye (*Stizostedion vitreum*) except those from the Sheep River (Shp) which were bull trout (*Salvelinus confluentus*). Lower case a / b divide populations into groups thought to be composed of mixed (may contain stocked or non-stocked) fish (a) and non-stocked fish (b). Numbers indicate bootstrap values.



Appendix 5. FITCH tree based on Nei's genetic distance values. All samples were walleye (*Stizostedion vitreum*) except those from the Sheep River (Shp) which were bull trout (*Salvelinus confluentus*). Lower case a /b divide populations into groups thought to be composed of mixed (may contain stocked or non-stocked) fish (a) and non-stocked fish (b). A distance ruler is provided at the base of the figure.